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18201 i ACO16814 Mus musculus clo
1519 i ACO20887 Mus musculus clo
1519 i ACO70284 Giardia intestinali
41 i AF090137 Homo sapiens carbo
58 i E16306 CDNA encoding kerata
96 i X98341 B.subtilis offRM1 DN
90 i U65637 Homo sapiens chondro
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9b_v1: AF208771

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9b_v1: AF325691

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-MODEL-frameh1.0FMT=fastap -SUFFTx=p2n.rge -GAPOP-12.000
-GAPDET-4.000 -MINMATCH=0.100 -LOOPCL=0.000 -KGAPEXT=0.500
-GAPDEXT=0.000 -GAPEXT=0.000 -YGAPOP-10.000 -XGAPEXT=0.500
-MODELEXT=7.000 -START=1 -MATRIX-blosum62
-FTRAMS-human40.cdi -IIST=-1000 -DOCALIGN=200 -THR_SCORE-pct
-THR_MAX=100 -THR_MIN=0 -ALIGN=50 -MODE-LOCAL -OUTFMT=pfs
-NORM-ext -MINNEN-0 -MAXLEN=200000000
-USRR-USO485559_@GGN1_1_4773 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLPXY
                                                                                              Results were produced by the GenCore software, version 4.5, Copyright (c) 1993-2000 Compugen Ltd.
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9b_htg:AC008336 9b_htg:AC028385 9b_htg:AC028385 9b_htg:AC028385 9b_htg:AC011448 9b_htg:AC011448 9b_htg:AC011448 9b_htg:AC01148 9b_htg:AC011352 9b_htg:AC011103 9b_htg:AC0213103 9b_htg:AC018119 9b_htg:AC011186 9b_htg:AC011186 9b_htg:AC011815 9b_htg:AC0118162 9b_htg:AC011815 9b_htg:AC0118162 9b_htg:AC0118162 9b_htg:AC0118162 9b_htg:AC01181862	9b htg: AC024276 9b_htg: AC020776 9b_rc: AC06014 9b_htg: AC08093 9b_htg: AC019180 9b_htg: AC019180 9b_htg: AC019180 9b_htg: AC02374 9b_htg: AC024967 9b_htg: AC024967 9b_htg: AC024967 9b_htg: AC024967 9b_htg: AC024967 9b_htg: AC026388 9b_htg: AC026388 9b_htg: AC026940 9b_htg: AC026940 9b_htg: AC026940 9b_htg: AC026940 9b_htg: AC026940 9b_htg: AC026940
2 of 4) of 6 of 8) of 6 of 8 of 8) of 6 of 86) of 6 of 36) of 8 of	AC024885 Homo sapiens clone AC024885 Homo sapiens chrome AC015539 Homo sapiens chrome AC074559 Mus musculus chrome AC074566 Homo sapiens chrome AC020598 Homo sapiens chrome AC013649 Homo sapiens clone AC012585 Homo sapiens clone AC012585 Homo sapiens clone AC07179 Homo sapiens clone AC07779 Homo sapiens labe cl AC07779 Homo sapiens labe cl AC07738 Homo sapiens labe cl AC07434 Homo sapiens clone AC07738 Homo sapiens clone AC07328 Homo sapiens clone AC07328 Homo sapiens clone AC07328 Homo sapiens clone AC07434 Human chromosome 14 AL1539186 Human chromosome 14 AL031558 Human pNA sequence
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00000000000000000000000000000000000000	733.14 733.04 733.04 722.09 722.09 722.09 722.09 722.77 722.77 722.77 722.77 722.77 722.77
9b_htg:AC09128B_1 9b_htg:AC09128B_1 9b_htg:AC09128B_2 9b_htg:LMFLCHR15_6 9b_htg:LMFLCHR15_6 9b_htg:LMFLCHR36_05 9b_htg:LMFLCHR36_05 9b_htg:LMFLCHR36_05 9b_htg:LMFLCHR36_05 9b_htg:LMFLCHR36_05 9b_htg:LMFLCHR36_13 9b_htg:LMFLCHR36_13 9b_htg:LMFLCHR36_13 9b_htg:LMFLCHR36_13 9b_htg:AL139143 9b_htg:AL139143 9b_htg:AL139163 9b_htg:AL139163 9b_htg:AL139255 9b_htg:AL139255 9b_htg:AL139255 9b_htg:AL161424 9b_htg:AC010112 9b_htg:AC010139 9b_htg:AC008496 9b_htg:AC008496 9b_htg:AC008496 9b_htg:AC008496 9b_htg:AC00843 9b_htg:AC008439 9b_htg:AC008439 9b_htg:AC008434 9b_htg:AC012334 9b_htg:AC012334 9b_htg:AC012334 9b_htg:AC016588 9b_htg:AC016586 9b_htg:AC018334 9b_htg:AC018336 9b_htg:AC018336 9b_htg:AC018369 9b_htg:AC018369 9b_htg:AC018369 9b_htg:AC018369 9b_htg:AC018369	882

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Eukaryoth viriliplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Booldeae; Triticae; Triticae.

1 (bases 1 to 1872)
Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M., Flintham,J.E., Beales,J., Fish,L.J., Worland,A.J., Pellaca,F., Fellacham, Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P., Green revolution' genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TAR242531 1872 bp DNA PLN 28-JUL-1999
Triticum aestivum rht-Dla gene for gibberellin response modulator.
AJ242531
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Submitted (25-MAX-1999) Richards D.E., Molecular Genetics, John
Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM
Location/Qualifiers
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Harberd, N.P., Peng, J. and Richards, D.E.
Green revolution genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         others
   HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
1. 453
/organism="Triticum aestivum"
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gibberellin response modulator; rht-Dla gene.
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Percent Identity: 100.000
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Ratio: 4.765
Percent Similarity: 100.000
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AC025999 Homo sapiens chromc
AC092711 Mus musculus clone
AC022875 Homo sapiens clone
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                      Homo sapiens
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticeae; Triticum.
1 (bases 1 to 453)
Harberd, N.P. and Peng,J.
Genetic control of plant growth and development
Patent: WO 9909174-A 66 25-FEB-1999;
                                                                                                                                                                                                                                                                                                                                          Embryophyta; Tracheophyta;
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( pasea 1 to 51)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development Patent: WO 9909174-A 105 25-FEB-1999;
HARBERO NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                        AL023693 I
AP003084 I
AC027725 I
AP001333 I
                    AC023830
AC090824
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189153
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Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:4565"
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Sequence 105 from Patent W09909174.
AX005896.1 GI:9928885
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AX005857
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US-09-485-529-104 x AX005896
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Ratio: 4.765
Percent Similarity: 100.000
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                                                                                                                                                                                    seq_name: gb_pat:AX005896
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LOCUS AX005896
DEFINITION Sequence 105
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gb_htg:AP003084
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gb_htg:AP001333
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9b_htg:AC023830
9b_htg:AC090824
9b_htg:AC029982
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24 - AUG - 2000

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; (Dosdeae; Triticae; Cobsectic Control of Plant growth and development Patent; Wo 9909174-A 3 25-FEB-1999; Patent; WO 9909174-A 3 25-FEB-1999; HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
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Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:4565"
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136
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769
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417
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556
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1444
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Sequence 3 from Patent WO9909174.
AX005794
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US-09-485-529-104 x AX005805
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Ratio: 4.765
Percent Similarity: 100.000
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LOCUS AX005794
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ESMLSELNAPPPPLPPAPQLNASTSSTVTGSGGYFDLPPSVDSSSSIYALRPIPSPAG
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases 1 to 2125)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 14 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      24-AUG-2000
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                                                                                                                                                                                                                                                                 /product="gibberellin response modulator"
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Gaps: 0
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/db_xref="taxon:4565"
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Sequence 14 from Patent W09909174.
AX005805
                                                                                                                                                                           /gene="rht-Dla"
/note="GAI ortholog"
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US-09-485-529-104 x TAE242531
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Percent Similarity: 100.000
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17 a 17

BASE COUNT ORIGIN

DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

AUTHORS REFERENCE

TITLE

JOURNAL

source

FEATURES

BASE COUNT ORIGIN

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alignment_block:
US-09-485-529-104 x AX005808
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US-09-485-529-104 x AX005807
                                      Quality: 78.00
Ratio: 4.588
Percent Similarity: 100.000
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Ratio: 4.588
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1 (bases 1 to 302)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 16 25-FEB-1999;
HARBERD NICHOLAS PAUL (EB); PENG JINRONG (GB)
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Gaps: 0
Percent Identity: 100.000
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LOCUS AX005807 302 bp DNA
DEFINITION Sequence 16 from Patent W09909174.
VERSION AX005807.1 GI:9928804
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/db_xref="taxon:4577"
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US-09-485-529-104 x AX005794
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Ratio: 4.765
Percent Similarity: 100.000
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae; Andropogoneae; Zea.
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                                                                                                                                                1 (bases 1 to 371)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 17 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
Gaps: 0 Percent Identity: 94.118
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Gaps: 0
Percent Identity: 94.118
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AX005808
AX005808.1 GI:9928805
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Sequence 12 from Patent W09909174.
AX005803
AX005803.1 GI:9928800
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a 121 c 139 g
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PIPSPVAAPSADPSTDSAREPKRMRTGGGSTSSSSSSSSSSSMDGGRTRSSVVEAAPPAT
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LOCUS AX005806 2255 bp
AX005806 Sequence 15 from Patent
ACCESSION AX005806
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US-09-485-529-104 x AX005806
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Ratio: 4.588
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                   Enkaryota: Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Shrhartoldeee; Oryzeae; Oryzea.

1 (bases 1 to 770)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 12 25-FEB-1999;
HARBERD NICHOLAS POUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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Zea mays partial d8 gene for gibberellin response modulator.
AJ242530
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/product="gibberellin response modulator"
/protein_id="CAB51557.1"
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Gaps: 0
Percent Identity: 94.118
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D8 gene; gibberellin response modulator.
Zea mays.
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/db_xref="taxon:4530"
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99347734

    1. .1890
    /organism="Zea mays"
    /db_xref="taxon:4577"

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Percent Similarity: 100.000
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panticoideae; Andropogoneae; Zea. 1 (bases 1 to 2255) Harberd, N.P. and Peng, J.
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Patent: WO 9909174-A 15 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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/db_xref="taxon:4577"
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us-09-485-529-104.p2n.rge

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to: AB030956 from: 1 to: 2500
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BARKVAAYEGBLARRYFERABSTLLDAAFBLLIHGESCPYLKESCPYLKERHETANGAI
LEAPKGCHRYHYDGEIKOGNOPALLOALLEPGGEPSFRLTGVGPPQPDETDALO
VGWKLAQFAHTIRVDFQYRGLVAATLADLEPFMLQPEGEADANEEPEVLAVVSVFELH
STLAQPGAHTIRVDFQYRRAIVTVVBQEANHINSGSFLDRFTESLHYYSTWEDSLEG
GSSGQAELSPPAGGGGTDDVMSEYVLGROICNVNVCEGABRTEHETLGOWRINLG
RAGFEPVHLGSNAYKQASTLLALFAGGGGYRVEKEKEGCLTLGWHTRPLIATSANRVA
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VESMLSELNAPLPP1PPAPPAARHASTSSTVTGGGGSGFFELPAAADSSSSTYALRP1
SLPVVATADPSAADSARDTKRMRTGGGSTSSSSSSSSLGGGASRGSVVEAAPPATQG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MKREYQEAGGSSGGGSSADMGSCKDKVMAGAAGEEEDVDELLAA
                                                                                                                                                                                                                                                                                                                                                    Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2 (bases 1 to 2500)
Sano, H., Ogawa, M. and Kusano, T.
Sano, H., Ogawa, M. and Kusano, T.
Direct Submission
Submitted (09-AUG-1999) to the DDBJ/EMBL/GenBank databases.
Mikhiro Ogawa, Nara Institute of Science and Technology, Plant
Molecular Breeding; Takayama 8916-5, Ikoma, Nara 630-0101, Japan
(E-mail: m-ogawa@bs.aist-nara.ac.jp, Tel:+81-743-72-5652,
                                                                                                                                                                                                30-MAR-2000
                                                                                                                                                                                                                                                                                                                                             Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Trach
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                       Oryza sativa (cultivar:Nipponbare) seedling cDNA to mRNA.
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308 GATGAGCTGCTGGCCGCCTCGGGTACAAGGTGCGTTCGTCGGATATGGC 357
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Gaps: 0
Percent Identity: 94.118
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Oryza sativa mRNA for OsGAI, complete cds.
AB030956

    .2500
    /organism="Oryza sativa"
    /cultivar="Nipponbare"
    /db_xref="taxon:4530"

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/db_xref="G1:6970472"
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216. .2093
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Percent Similarity: 100.000
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US-09-485-529-104 x AB030956
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                                                                                                                             seq_name: gb_p1:AB030956
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                                          17 a 17
                                                                                                                                                                                                LOCUS
DEFINITION
                                                                                                                                                                                                                                                                                                       SOURCE
ORGANISM
                                                                                                                                                                                                                                    ACCESSION
VERSION
KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                REFERENCE
AUTHORS
TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         JOURNAL
MEDLINE
REFERENCE
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JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AUTHORS
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Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genscan+ (Chris Burge, http://www.softberry.com/), http://CRr081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org/, searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tgl.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity but with EST similarity to other proteins are named similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, CANASCAN-SE). Simple repeats are indentified by repeatmasker (Arian Smit, http://encome.wustl.edu/eddy/tRNAscan-SE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzaae; Oryzaa.

1 (Joases I to 122497)

Buell,C.R., Yuan,Q., Ouyang,S., Moffat,K.S., Hill,J.N.,
Gansberger,K., Brenner,M., Burgess,S., Hance,M., Shvartsbeyn,M.,
Valitin,T., Riggs,F., Hsiao,J., Zismann,V., Blunt,S., Pai,G.,
VanAken,S.E., Utterback,T.R., Feldblyum,T.V., Quackenbush,J.,
Salzberg,S.L., White,O. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (25-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr, Rockville, MD 20850, USA
3 (bases 1 to 122497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (20-APR-2001) The Institute for Genomic Research, 9712 Medical Center Dr. Rockville, MD 20850, USA (bases 1 to 122497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BAC clone OSJNBb0022E02 is from Oryza sativa chromosome 3
The orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                           seq_documentation_block:
LOCUS AC087797 122497 bp DNA PLN
DEFINITION Oryga sativa chromosome 3 BAC OSJNBb0022E02 genomic sequence,
complete sequence.
ACCESSION AC087797
VERSION AC087797.5 GI:13699786
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Direct Submission
Submitted (03-MAY-2001) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
Medical Contest Dr. Rockville, MD 20850, USA, rbuell@tigr.org
Address all correspondence to:rice@tigr.org
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Location/Qualifiers
(bases 1 to 122497)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Direct Submission
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gene mRNA

CDS

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// In the complement (2544 ... 2588)
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// pt_family="Ar_rich"
// pt_family="(GGAGAA)n"
// pt_fa
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LYIMEQFHDYKMADNRSVVEQAHEIQTMAKELELLKCVLPDKFVAGCIIAKLPPSWRS
                                                                                                                                                                                                                                                                                                                                                                                                                                           GNTGDGSGYGRTGFHRPNGEMVTCFCSWCWHGRSEVYFGKDRAAEERAACPFYRQESC
YECGGLFRFSLSDFCNKSVNHICGSVDDEANVWHSRLCHINFGLMSRLSSMCLIPKFS
IVKGSKCHSCVQSKQPRKPHKAAEERNLAPLELLHSDLCEMNGVLTKGGKRYFWTLID
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            DATRECYVILKTKIEALDYFKIYKAEVENOLDRKIKRLRSDRGGEFFSNEFDLFCEE
HGIIHERTPPYSPESNGIAERKNRTLTDLVNAMLDTAGLPKAWWGEALLTSNHVLNRV
PNRNKDKTPYEIWIGRKPSLSYLRTWGCLAKVNVPITKKRKLGPKTVDCVFLGYAHHS
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complement(22507). .22529)
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SPIGLLPTRRLRCQYSTGSLPESAAGHAVATPRSPSRRPGADAADEGEVLGLSSAAAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WMGAQARSGCEGNÄESMAVALSACPYAGDLALAKGEATHGCGVMKGVIHGYVFTTNSL
VCMYGKLGEMDNAKKAFRDATEKNIVTWNTLITSYATAGLCDEALDVLAQMEQIGGTV
                                                                                                                                                                                                                                                                                                                                                                FGTALKHKRQEYSVEGLIASLDVEEKAREKDAASKGDGGGSSANVVHKAQNKSKGKYK
AQQTTNFKKQKKNNNNPNQDERTCFVCGQVGHLARKCPQRKGMKAPAGQTSKSANVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      YPAVLEGYSDSNWISDVDEIKATSGYVFTLGGGAVSWRSCKQTILTRSTMEAELTALD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TATVEAEWLRDLLMDLPVVEKPTCEKT IEVCQEIKKLRSYNVGLHPNSEKPGRSLHEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      IITKCDRQCIEGDGFETHSILEGTHLCELDCWSQSMKILGESSRKLTKDLGV
                                                                                                                 t="putative gag-pol polyprotein"
n_id="AAK50117.1"
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Gaps: 0
Percent Identity: 94.118
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /note="predicted by fgenesh"
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complement(19612. .19640)
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complement(20459. .20487)
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21271. 21576
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /translation="MRASVETGVHSNVPLERVRQLGATLRPGCSSGGARNVGRGSTAA
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EEVWRLQAALGEQSEITKCTKQEFERLQNEKVLCRICYEGEICMVLLPCRHRTLCKTC
SDKCKKCPICRVPIEERMPVYDV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="hypothetical protein"
/protein_id="AAK50133.1"
/db_xref="G1:13937302"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     join(<14168. 15023,15131. .1.
17887. .18048,18262. .>18366)
/gene="OSJNBb0022E02.12"
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/rpt_family="(GA)n"
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                                                                                                                                                                                                                                                                                                                          complement(<1271. .>1579)
/gene="OSJNBb0022E02.11"
                                                                                                                                                                                                                                                                                                                                                                                                     complement(1271. .1579)
/gene="OSJNBb0022E02.11"
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/gene="OSJNBb0022E02.18"
1386. .1640
/gene="OSJNBb0022E02.18"
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/gene="OSJNBb0022E02.18"
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                                         /organism="Oryza sativa"
                                                                       /cultivar="Nipponbare"
/sub_species="japonica"
/db_xref="taxon:4530"
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Arabidopsis thaliana Eukaryothyta; Embryophyta; Tracheophyta; Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots.
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 1931).
Truong, H. N., Caboche, M. and Daniel-Vedele, F. Sequence and characterization of two Arabidopsis thaliana cDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant FEBS Lett. 410 (2-3), 213-218 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
de Biologie Cellulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
FRANCE
                            Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta; Wildiplantae, Streptophyta; Enkaryothyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldees; Triticum.

1 (bases 1 to 324)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development Patent: WO 9909174-A 76 25-FEB-1999; HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                             3 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /dev_stage="two-leaf stage seedlings"
/note="Landsberg erecta ecotype"
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Percent Identity: 100.000
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"Organism="Arabidopsis thaliana"

/sub_species="(L). Heynh"

/db_xref="taxon:3702"
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/organism="Triticum aestivum"
/db_xref="taxon:4565"
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/gene="RGA2"
196. .1794
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US-09-485-529-104 x AX005867/rev
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Truong, H.N.
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                   Triticum aestivum
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Percent Similarity: 100.000
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Oryza sativa.

Oryza sativa

Oryza sativa

Eukaryota; Viridiplantae: Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 725)

Harberd, N. P. and Peng, J.

Genetic control of plant growth and development Patent: WO 9909174-A 19 25-FEB-1999;

HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)

Location/Qualifiers
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Gaps: 0
Percent Identity: 93.750
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/db_xref="taxon:4530"
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Ratio: 4.500
Percent Similarity: 100.000
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                                                 /protein_id="Ca72178".
//protein_id="Ca72178".
/db_xref="C1:2339980"
/db_xref="C1:233980"
/db_xref="C1:
                                                                                                                                                                                                                                                                                                                                                                                                                    VACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALENGGEGYRVEES
DGCLMLGWHTRPLIATSAWKLSTN"
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1 (bases 1 to 1964)
Harberd, N.P., Peng, J., Carol, P. and Richards, D.E.
NUCLEIC ACID ENCODING GAI GENE OF ARABIDOPSIS THALIANA
PATENT: WO 9729123 A 114-MG-1997;
INNES JOHN CEMTRE INNOV LID (GB)
Other publication AU 1799697 19970828.
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Gaps: 0
Percent Identity: 82.353
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Sequence 1 from Patent W09729123.
A64697
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/codon_start=1
/product="RGA2 protein"
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/haplotype="GAI"
426 c 474
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis thaliana
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Ratio: 4.118
Percent Similarity: 100.000
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Percent Similarity: 100.000
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LOCUS A64697
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Ratio:
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/translation="MKRDHHHHQDKKTMMMNEEDDGNGMDELLAVLGYKVRSSEMAD VAQKLEQLEYVMLSVRYOEDDLSQLATEVHYNPAELYTWLDSMLTDLMPPSSNAETDLK ALGDALLNOFALDSMLSVNOGGGDTTTWRLKCSNGVVETTTATAESTRHVVLVD SQENOYRLYHALLAGAEAVOKANLTYMEALVKQIGFLAVSQLGAMRKVATYFAEALAR RIYRLSPSQSPIDHSLSDTLQMHFYETCPYLKFAHFTANQAILEAFQGKKRVHVIDFS
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STGFVANTTABLDASMLERRSEIESSANNSYFELHKLLGRPGAIDKYLGVVNGIKP
EIFTVVEGESHHNSPIFLDRFFESLHYYSTLEDSLEOVPSGORVWSEYVLGKQICNV
VACDGPDRVERHETLSQWRNRFGSAGFAAAHIGSNAFKQASMLLALFNGGEGYRVEES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; thaliana
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 1964)
Peng, J., Carol, P., Richards, D.E., King, K.E., Cowling, R.J.,
Murphy, S.P. and Harberd, N.P.
The Arabidopsis GAI gene defines a signalling pathway that
negatively regulates gibberellin responses
Genes Dev. In press
2 (bases 1 to 1964)
Harberd, N.P.
Harberd, N.P.
Harberd, N.P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Direct Submission
Submitted (22-OCT-1997) N.P. Harberd, John Innes Centre, Molecular
Genetics, Colney Lane, Norwich, NR4 7UJ, UK
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                   01-NOV-1997
                                                                                                                                                         287 GATGAGCTTCTAGCTTCTTGGTTACAAGGTTAGGTCATCGGAAATGGC 336
                                                                                                                              1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                      PLN
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Percent Identity: 82.353
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/orqanism="Arabidopsis thaliana"
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/db_xref="taxon:3702"
/chromosome="1"
209. 1807
/gene="GAI"
209. 1807
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/db_xref="GI:2569938"
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                                                                           to: 1964
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/gene="GAI"
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Arabidopsis thaliana
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Y15193.1 GI:2569937
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US-09-485-529-104 x ATY15193
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Percent Similarity: 100.000
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alignment_block:
US-09-485-529-104 x A64697
                                                                        Align seg 1/1 to: A64697
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LOCUS ATY15193
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thale cress.
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273 GATGAGCTTCTCGCTGTTTTAGGTTACAAAGTTAGGTCATCGGAGATGGC 322
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Percent Similarity: 100.000
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US-09-485-529-104 x ATRGA1
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LOCUS
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ORIGIN
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KEYWORDS
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AUTHORS
TITLE
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AUTHORS
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VRLVHALMACAEAIQQNNLTLAEALVKQIGGLAVSQAGAMRKVATYFAEAEARRIYRL
SPPQMOIDHCLISDTLQMHFYETCPYLKFAHFTANQAILGEREKKRVHYIDFSMNGL
OMALMQALALREGGPPTRIJGIGPAPDNSDHLHEVGGKLAQLAEAVHVEFEYRGF
VANSLADLDASMLERRSDFERVANNSVFELHKLLGREGIEKVLGVVKQIKPYFFY
VEQESNHNGPVFLDRFTESLHYYSTLFDSLEGVPNSQDKVMSEVYLGKQICNLVACEG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation-"MKRDHHQFQGRLSNHGTSSSSSISKDKWMVKKEEDGGGNMDD
ELLAVLGYKVRSSEMAEVALKLEQLETMMSNVQEDGLSHLAADTVHYNPSELYSWLDN
MLSELNPPPLPASSNGLDPVLPSPEICGFPASDYDLEVIPGNAIYQFPAIDSSSSSNN
                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;

Bermatophyta; Magnollophyta; eudicotyledons; core eudicocts;

Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 2201)

Peng, J., Carol, P., Richards, D. B., King, K. B., Cowling, R. J.,

Murphy, G. P. and Harberd, N. P.

The Arabidopsis GAI gene defines a signalling pathway that negatively regulates gibberellin responses

2 (bases 1 to 2201)

Harberd, N. P.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Direct Submission Submission Submitted (22-007-1997) N.P. Harberd, John Innes Centre, Molecular Genetics, Colney Lane, Norwich, NR4 7UJ, UK
                                                                                                                                                                                                                                                                         01-NOV-1997
                                                        1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                           PLN
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Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                       ATY15194 2201 bp mRNA ATADIdopsis thaliana mRNA for GRS protein.
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/strain="Columbia"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /product="GRS protein"
/protein_id="CAA75493.1"
/db_xref="G1:2569940"
/db_xref="SPTREMBL:023725"
                      to: 1964
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                    to: ATY15193 from: 1
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144. .1907
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/codon_start=1
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Percent Similarity: 100.000
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                    Align seg 1/1
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ACCESSION
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KEYWORDS
SOURCE
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MLSELNPPLPASSNGLDPVLESPETGGFPASDYDLKYTFGNATYOFPAIDSSSSSNN
QNRRLKSCSSPDSWYTSTSTGTOLGGVLGTYVTTTTTTTAAABSTREVILVDSOENG
VRLYHALMACABAIQONNLTABALVKOIGCLAGAARKVATYFABAABSTREVILVDSOENG
VRLYHALMACABAIQONNLTABALVKOIGCLAGAARKVATYFABABATRYTL
SPPQNOIDHGLSDTLCAHFYFTCPTGCPTLKFAHFTANQAILBAFBCKKRYHYIDESHNOGL
QWPALMQALALREGGPPTFRLTGIGPPAPDNSDHLHBVGCKLAQLABAIHVEEYRGF
VNSLAADLDASMLELRRSDTBAVANVONYFELHLKLGRPGGIRCYLGVYGIRVYIFTV
VROGENHNGYPYLDRFTBSLHYTSTLFBDLEGVPNSQDRVMSEVTLGKQICKILVACGG
PDRVERHETLSQWGNRFGSSGLAPAHLGSNAFKQASMLLSVFNSGQGYRVEESNGCLM
                                                                                                                                                                                                                                                                                                                                                                                                                                         Truong, H.N.
Direct Submission
Submitted (13-FEB-1997) H.N. Truong, INRA-Versailles, Laboratoire
de Biologie Cellulaire, Route de Saint-Cyr, 78026 Versailles Cedex,
FRANCE
                                                                                                                                                                                                                                                                                 1 (bases 1 to 2210)
Truong, H.N., Caboche, M. and Daniel-Vedele, F.
Sequence and characterization of two Arabidopsis thaliana cDNAs isolated by functional complementation of a yeast gln3 gdh1 mutant FEBS Lett. 410 (2-3), 213-218 (1997)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /translation="MKRDHHQFQGRLSNHGTSSSSSSISKDKMMMVKKEEDGGGNMDD
ELLAVLGYKVRSSEMAEVALKLEQLETMMSNVQEDGLSHLATDTVHYNPSELYSWLDN
                                                                                                                                                                                                                 Tracheophyta;
      19-AUG-1997
                                                                                                                                                                                                        Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheof
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids II; Brassicales, Brassicaceae, Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /dev_stage="two-leaf stage seedlings"
         PLN
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1. .2210
/organism="Arabidopsis thaliana"
/sub_species="(L). Heynh"
/db_xref="taxon:3702"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /product="RGA1 protein"
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ATRGAL 2210 bp MRNA A.thaliana MRNA for RGAl gene. Y11336.1 GI:2339977 RGAL gene. thale cress.
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132. 1895
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join(90. .236,706. .858,954. .1017,1270. .1349,1432. .1579, 1936. .1997,2237. .2299,2675. .2733,3037. .3118,3204. .3247, 3335. .3559,3638. .3656)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Arabidopsis thaliana Arabidopsis thaliana Sukaryota; Bmbryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis. (Dases 1 to 24604)
Sato,S., Nakamura,Y., Kaneko,T., Kato,T., Asamizu,E., Kotani,H., Tabata,S., Mewes,H.W., Rudd,S., Lemcke,K. and Mayer,K.F.X.
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EU Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

EU Arabidopsis sequencing, project.

Euch Submission

Submission

Submission, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Biochemie, Am Klopferspitz 18a, D-82152 Martinsried, FRG, E-mail:

Iemcke@mips.biochem.mpg.de,mayer@mips.biochem.mpg.de

Information on performance of analysis and a more detailed

annotation of this entry and other sequences of chromosomes 3, 4

and 5 can be viewed at: http://www.mips.biochem.mpg.de/proj/thal/.

Location/Qualifiers
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Arabidopsis thaliana DNA chromosome 5, BAC clone K3M16 (ESSA
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Gaps: 0
Percent Identity: 82.353
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/organism="Arabidopsis thaliana"
/variety="Columbia"
/db_xref="taxon:3702"
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90. 226
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90. .3656
                                           /number=3
1530. .1880
/gene="SCR2"
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1434. .1529
/gene="SCR2"
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1881. .3410
/gene="SCR2"
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Quality: 70.00
Ratio: 4.118
Percent Similarity: 100.000
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/ Ob_xref="(STERBL:065367"
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LSDETVYHYNDSGUSSWTSPLOFTRIQERPOSEYDLRAIPGSAVVRDEHVYRRS
KRTEIESELSSTRSVVVLGSGETGYRLVHALLACARAVQONNIKLADALLVKHVGLLAS
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GWRLGQLASTIGVNFEFKSIALNUSDLKFPELLHYSSLEDSLGFSPSQDRV
MSGLEGRRYTARKYROPGRANNINGTVFLDRFTESLHYSSLEDSLEGPPSQDRV
MSGLEGRRYTARKYROPGRANNINGTVFLDRFTESLHYSSLEDSLGFSPSQDRV
MSGLEGRRYTARKYROPGRANNINGTVFLDRFTESLHYSSLEDSLGFSPSQDRV
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Eukaryota; Viridiplantae; Streptophyta; Eudicotyledons; core eudicots;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

[ (bases 1 to 4081)
Sanchez-Fernandez, R., Ardiles-Diaz, W., Van Montagu, M., Inze, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Submitted (14-MAR-1998) Sanchez-Fernandez R., Department of Genetics, University of Gent (VIB), K.L. Ledeganckstraat 35, 9000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:3702"
join(900. 1048,1130. 1343,1434. 1529,1881. 3410)
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1434. 1529,1530. 1880,1881. 3410)
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/gene="SCR2"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Cloning of the Arabidopsis thaliana RGA-like gene, a putative member of the VHIID domain transcription factor family
                                                                                                                                                                                                                                                         19-MAY-1998
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                        1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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/number=2
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Sanchez-Fernandez, R.
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/note="similarity to cisplatin resistance-associated overexpressed protein - Homo sapiens, EMBL:AB034205" /codon_start=1 /potein - Homo sapiens, EMBL:AB034205" /codon_start=1 /proteir=relive protein" /proteir=relive protein" /protein_id="CAC01888.1" /db.xref="Cal:9755768" /translation="MDAMRKQLDVLMGANRNGDVTEVNRKYYDRDVCRLYLSGLCPHE LFQCIPAGVDNYDREEDALIPPERTOSP EILELSKQIKEKKEADLHOLGGKTDLKTRALELVEEMRTRRADLQAVLLLDAFNKDR TSLQQAVPAQOPAATLAPPDPRTQEMINEKLKKABELGGEGGGGWNDEAQKALICAPROTERRERSEREGGGGGGGGGGGGGGGGGGGGGGGGGGGGGG	237705 237705 .7gene=1.78/M16_10*	706858 /gene="K3M16_10" /number=2	/gene="K3M16_10" /number=2 /9541017		1270 . 1349 /gene="K3M16_10" /number=4	13501431 /gene="K3M16_10" /number=-4	14321379 /gene="K3M16_10" /numbe=5 15801935	/gene="K3M16_10" /number=5 19361997	/gene="K3M16_10" /number=6 19982236 /gene="K3M16_10"	/numer=6 2237 2299 /gene="K3M16_10" /number=7 2300 5.674	/gene="K3M16_10" /number=7 2675. 2733 /gene="K3M16_10"	27343036 /gene="K3M16_10" /number=8	303/. :3118 /gene="53M16_10" /number=9 3119. :3203	/gene="K3M16_10" /number=9 3204. 3347		/number=10 3335, .3559 /gene="K3M16_10" /number=11
	intron	exon	exon	intron	exon	intron	futron	exon	intron	exon	exon	intron	exon intron	exou	intron	exon

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Counces were identified by a combination of three methods: Gene prediction programs including GRAIL (available by anonymous ftp from arthur repm.orn.] gov), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://gnomic.stanford.edu/-chris/GENSCANW.html), searches of the (http://www.cbs.dtu.dk/netpgene.html), searches of the complete sequence against a peptide database and the Arabidopsis EST database at TIGR (http://www.tigr.org/tdb/at/at.html).

Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, the simple repeats are identified by repeatmasker (Arian Smit, thtp://ftp.genome.wastl.edu/eddy/tRNAscan-SE/). Simple repeats are identified by repeatmasker (Arian Smit, thtp://ftp.genome.wastlnigton.edu/RW/RepeatMasker.html). Regions of genomic sequence that are nonctated as genes but have predicted exons by GRAIL are annotated as misc features.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /protein_id="AAF01600.1"
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LFIIISDSSYYKRNICGARKGEPAALLLSSSNNEWASTLATSDFSRQPSGSLTIFLTSP
VQAFCLLREISCRAVLALYTPVENNKQNOPECCPSLPESLLDTAPPWSQILKDPFLR
RLLLRFIFCRAVLALYTPVENNKQNOPECCPSLPESLLDTAPPAVQSAVEQMANVEGAT
SKFTIPQDITMLESF"
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join(3627. 3661.3762. 3843.3918. 3895.4081. 4140,
4240. 4344.4437. 4547,4629. 4670,4860. 4973,5097. 5254,
5361. 5494.5576. 5682,5785. 5827,5903. 6144)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1. .24217
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(AC009327:65718. .89934)."
complement(join(88. .215,451. .587,675. .857,959. .1050,
1459. .1593_1682. .1748,1837. .2055,2146. .2340,2492. .2879,
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orientation of the sequence is from SP6 to T7 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /hote="similar to hypothetical protein GB:CAB38918
[Arabidopsis thaliana]"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1. .82289
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/cultivar-"Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="unknown protein"
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/gene="T21P5.1"
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Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B., Ronning,C.M., Koo,H., Fujii,C.Y., Oltterback,T.R., Barnstead,M.E., Arabidopsis, thaliana chromosome III BAC T21P5 genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   9712 Medical Center Dr.
Rockville, MD 20850, USA
e-mail: xlin@tigr.org
BAC clone T21P5 is from Arabidopsis chromosome III and is near the
molecular marker mi172.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Submitted (24-JAN-2001) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA On Jan 24, 2001 this sequence version replaced gi:12280866. Address all correspondence to:
                                                                                                                                                                                                                                                                                                                    /gene="K3M16_40"
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/note="strong similarity to calmodulin-related protein
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS ATAC009895 82289 bp DNA PLN 24-JAN-2001
DEFINITION ARADIdopsis thaliana chromosome III BAC T21P5 genomic sequence,
complete sequence.
ACCESSION AC009895
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            16029 GACGAGTTTCTTGCTGTTTTGGGTTACAAGGTTCGATCTTCAGACATGGC 15980
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality: 70.00 Length: 17 Ratio: 4.118 Gaps: 0 Percent Similarity: 100.000 Percent Identity: 82.353
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The Institute for Genomic Research
                                                                                                                                             complement(11207. .11647)
                                                                                                                                                                                                                                       complement(11207. .11647)
complement(9143. .9680)
                                                             .9866)
                                                       complement(9681.
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                                                                                                                                                                            /gene="K3M16_40"
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US-09-485-529-104 x ATK3M16/rev
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                                                                                                                  /number=5
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complement(14488 . .14563)
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VRVPTFFISPPIEDFTLANDRYGRFYDHYBYKIFKLEKRDSWAGT
FESVITRNSPRQDCFPTLSNPYKMRGYVAKENSLENDFOCEELVIVAAGLKGDYKNEEL
LYKLCKKTCVSDASKYVTKAFDKFVEESKKARERGGDENDIVFCVDDDDDHNVVKPPP
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 85702)
Lin,X., Kaul,S., Town,C.D., Benito,M., Creasy,T.H., Haas,B.J.,
Wu,D., Maitl,R., Ronning,C.L., White,O., Nierman,W.C. and Fraser,C.M.
Arabidopsis thallana chromosome 1 BAC T27F4 genomic sequence
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (08-3M-2000) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, xlin@tigr.org 3 (bases 1 to 85702)
TOWN,C.D. and Raul,S.
Direct Submitsed (19-3M-2001) The Institute for Genomic Research, 9 Medical Center Dr. Rockville, MD 20850, USA, cdtcwn@tigr.org on Jan 19, 2001 this sequence version replaced g1:12280876.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         38963 GATGAGCTTCTTGCTGTTCTTGGCTACAAGGTTCGATCTTCTGAGATGGC 39012
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Gaps: 0
Percent Identity: 82.353
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Lin, X. and Kaul, S.
Direct Submission
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Ratio: 4.118
Percent Similarity: 100.000
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement(10838. .10896)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              .12578,12676. .13085,13162. .13332,
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DQLQWKTKACNDRIRELSSIVENQPGTDFISKDNHDPRNSKTQASYGSTDRGNDYQTN
                                                                                                                                                      EQLLPPMENVTRNPYHNIMODTESLRFNNQIGGGSOGIFPOPKRENFGYPLSSVAGKE
MOGREBEKABNSAMPDAYNONBEFASHYVEBGFGTIOFPOITOBAIPGEKVLGCGFPVR
MTTLCMFGWYRHLEDGTROYIEGARHPEYIVAADDVDKLIAVECIPMDDQGRQVKYRD
FSGIYSFNESVVSKDVLLIMOGELVRLFANDONKIRCGNVFNGT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /translation-"MGSTGNPNPWGTTYDSYRDCSQGVCSVYCPQWCYVIFPPPPSFY
LDDEDDSSSSSEPSPLLIALIGILASAFILVSYYLLISKYCHRRHNSSSTSAAAINRI
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/rote="excan predicted by xgrail, quality good_shadowexon"
8054. 8113
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/gene="T21P5.3"
/gene="T21P5.3"
/gene="T21P5.3"
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                                                                                                                                                                                                                                                                                                                                   excellent"
                                                                                                                                                                                                                                                                                                                                                                                    excellent"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /note="exon predicted by xgrail, quality marginal" 8263. 8380
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complement(8592. 8627)
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marginal_shadowexon"
e8652. >9527
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                                                                                                                                                                                                                                                                                                                                                                                                                                     quality marginal"
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                                                                                                                                                                                                                                                                                                                                   /note="exon predicted by xgrail, 6794. .6839
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8652. .9
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/rpt_family="SIMPLEGUX1|SIMPLEGUX1|SIMPLEGUX1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simplegux1|simpleg
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/rpt_family="SimpleGuY1|SimpleGuY1 SimpleGuY1 is a consensus."
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complement(7286. 7355)
                                                                                                                                                                  Complement(7001. 7085)
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complement(7036. .7205)
/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          complement(7038. .7208)
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                        DNA transposon - a consensus."
                                                                                                                                     putative non-autonomous DNA transposon - a consensus."
                                                                        complement(6991. ./205)
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Genes were identified by a combination of several methods: Gene prediction programs including Genscan+ (Chris Burge, http://CCR-081.mit.edu/GENSCAN.html), GeneMarkHMM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), GlimmerA (a variant. of GlimmerM, see Mihaela Pertea, du/GeneMark/), GlimmerA (a variant. http://www.tigr.org/softlab/glimmerM.htm], GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mpertea@tigr.org), searches of the complete sequence against a peptide database and the plant EST database at TiGR (http://www.tigr.org/tdb/tgi.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity are named as unknown proteins. Genes without proteins over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE (Sean Eddy, http://genome.wustl.edu/eddy/tRNAscan-SE).

Location/Qualifiers

Location programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.washington.edu/RW/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(<1757, .1964,2044, .2152,2244, .2346, 2351, 2243, .2346, 2431, .2465,2573, .2790,2869, .2984,3105, .3357,3447, .3534, 3625, .3702,3870, .3945,4033, .4088,4206, .4275,4478, .>4642))
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="similar to GB:AAB64244 from [Arabidopsis thaliana]
(Plant Mol. Biol. 34 (1), 57-68 (1997))"
complement(join(1757. 1964, 2044. 2152,2244. 2346,
2431. 2465,2573. 2790,2869. 2984,3105. 3357,3447. 3534,
3625. 3702,3870. 3945,4033. 4088,4206. 4275,4478. 4642))
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FEPHDLKDSNDAPTVSRVLDFMLGWHLEPTTSGDYPQIMKDLLGYRLPQFTAAQKAKL
KDSTDFVGLNYYTSTFSNYNEKPDPSKPSWKQDSLVSWEPKNVDHSAIGSMPLTAALP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /translation="MALQKFPLMGLLLLTILVSVTTAVDDPVCPATSKLSRASFPNG
FLFGTATAAFQVEGAINETCRGPALMDIYCRRNPERCSGDHADVAVDFFHRYKEDIQL
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FLAQGVRPSALKRDEL"
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            complement(6981. .7112)
/rpt_family="SIMPLEGUX1|SIMPLEGUX1 is a putative non-autonomous DNA transposon - a consensus."
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a putative non-autonomous DNA transposon - a consensus."
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 SIMPLEGUY1 is a
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/rpt_family="SIMPLEGUY1|SIMPLEGUY1 is a
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/db_xref="GI:12324390"
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/gene="T27F4.2"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /cultivar="Columbia"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /clone="T27F4"
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Genes were identified by a combination of three methods: Gene prediction programs including GRAIL (ftp://arthur.epm.orn.jeov/pub/xgrail), Genefinder (Phil Green, University of Washington), Genscan (Chris Burge, http://archur.epm.orn.jeov/pub/xgrail), and NetPlantGene http://www.cbs.dtu.dk/services/RetGene2/), searches of the complete sequence against a peptide datebase and plant EST databases at TIGR, and manual curations based on those analyses. Annotated genes are named to indicate the level of evidence for their annotation. Genes with similarity to other proteins are named after the database hits. Genes without significant peptide similarity but with EST similarity, that are predicted by two or more gene prediction programs over most of their length are annotated as 'hypothetical' proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, http://genome.wasth.edu/eddy/tRNAscan-SE). Simple repeats were identified by repeatmasker (Arian Smit, http://ftp.genome.washington.edu/RW/RepeatMasker.html). Genes are numbered from the top to bottom of the chromosome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                We thank the CSHL/WashU/ABI consortium for sequencing BAC clones F6P23, F5J6, T17A5, and T13L16, the ESSA group for sequencing clone F13D4, and Scott Jackson, Jiming Jiang, Klaus Meyer, Eric Richards and Satoshi Tabate for helpful assistance. In addition, we would like to thank the TIGR Bioinformatics Department, especially Lixin Zhou, Hanif Khalak, Michael E. Heaney, Lily Fu, Feng Liang, Jeremy Peterson, Michael Holmes, and Delwood Richardson for software and database support.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LAFDYSLEWGIHLKKSAYLALIGNFIRSNELPKVIEVVKEMVKAQHSLGCYQCAMLIH
RLGFGRRPRLAADVFDLLPDDQKGVAAYTALMDVYISAGSPEKAMKILREMREREIMP
SLGTYDVLLSGLEKTSDFQKEVALLRKEKKSLVASARFRENVHVEDKICDLLFATNLL
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On Dec 17, 1999 this sequence version replaced g1:3785968. The sequence and annotation of chromosome 2 were merged from those of the individual clones on this chromosome after removing overlaps. For detailed information, please see the TIGR web site (http://www.tigr.org/tdb/at/at.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             This work was supported by the National Science Foundation,
Department of Energy and the US Department of Agriculture.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                <341. .>997
/gene="AL2g01390"
/note="F219.1; predicted by genscan"
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/gene="At2g01400"
/note="F219.2; predicted by genscan"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        at@tigr.org
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/note="Sequence from clone F10A8"
301. .>95137
/note="Sequence from clone F219"
<341. .>997
/gene="At2g01390"
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/cultivar="Columbia"
/db_xref="taxon:3702"
/chromosome="II"
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join(<1175. .1294,1620. .>1940)
/gene="At2g01400"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           complement(1085. .1127)
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Location/Qualifiers
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         COMMENT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(<14953. .15216,15304. .15444,15534. .>16490))
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AC005560.2 GI:6598472
HTG.
                                                                                                                                                /db_xref="G1:10021".
//db_xref="G1:10021".
//translation="walQkPPLGLELFLTIVVSSTIAVDDPVCPTTSKLSRASFPNG
//translation="walQkPPLGLELFLTIVVSSTIAVDDPVCPTTSKLSRASFPNG
PVFGPATAAAPQVBGAINETCRRPADADIFCKRANDSVADFPRENEXDIQL
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TPQDLEDEYGGFLSENIVKDFREYADVVFTEYGGKVKNWITPFNEPWYPAHACYDVGKR
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VYAKGFRSLLKYIKDKYANPEIMIMENGYGDKLKDKDSVEVGTADYNRKYYLQRHLLA
                                                                                                                                                                                                                                                                                                                                                                                                                                 MNEAICIDKVRVTGYFVWSLLDNFEWQDGYNNRFGLYYVDFKNNLTRYEKESAKYYKD
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Lin,X., Kaul,S., Rousley,S.D., Shea,T.P., Benito,M.-I., Town,C.D.,
Eujij,C.Y., Mason,T.W., Bowman,C.L., Barnstead,M.E.,
Feldblyum,T.V., Buell,C.R., Ketchum,K.A., Lee,J.J., Ronning,C.M.,
Koo,H., Moffat,K.S., Cronin,L.A., Shen,M., VanAken,S.E., Umayam,L.,
Tallon,L.J., Gill,J.E., Adams,M.D., Carrera,A.J., Creasy,T.H.,
Goodman,H.M., Somerville,C.R., Copenhaver,G.P., Preuss,D.,
Nierman,W.C., White,O., Eisen,J.A., Salzberg,S.L., Fraser,C.M. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Arabidopsis thaliana
Eukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Submitted (09-MAR-2000) The Institute for Genomic Research, 9712 Medical Center Dr., Rockville, MD 20850, USA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="contains Pfam profile: PF00646 F-box domain"
                                                                                       /product="beta-glucosidase, putative; 11384-8406"
/protein_id="AAG52159.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 17
Gaps: 0
Percent Identity: 82.353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /gene="T27F4.4"
complement(14953. .16490)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                FLGQGVRPSALKKDEL"
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      11220. .11384))
/gene="T27F4.3"
                                                                 /codon_start=1
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Percent Similarity: 100.000
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US-09-485-529-104 x AC020665
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Arabidopsis thaliana
Arabidopsis thaliana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bosidae; Eurosids II; Brassicales; Brassicaceae; Arabidopsis.
I (bases I to 13269)
I (bases, J. Shinn, P., Dunn, P., Buehler, E., Kahn, S., Kim, C., Walker, M., Williams, S., Altafi, H., Araujo, R., Conn, L., Conway, A.B.,
Gonzalez, A., Hansen, N.F., Huizar, L., Kremenetskala, I., Lenz, C.,
Li, J., Liu, S., Luros, S., Rowley, D., Schwartz, J., Toriumi, M.,
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PANMOPIPKEITKVFGLPSLNDAYVGIHEPKTLDEADLARKRLIFDEFFYLQLARLYO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         MLQSLGTK I EKDVLLEKFRK PVLNSVY I EEWSTLTKSFLKALPYSLTPSQLŠAVSET I
WDLKRPVPMNRLLQGDVGCGKTVVAFLACMEV I GSGYQAAFMAPTELLA I QHYEQCRD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LLENMEGDLQSGAISFIIGTHSLIAEKIEYSALRIAVVDEQORFGVIQRGKFNSKLYG
TSMISKSGSSDSDDTSKADLSMAPHVLAMSATPIPRSLALALYGDISLTQITGMPLGR
IPVETHIFEGNETGIKEVYSMMLEDLKSGGRVYVVYPVIDQSEQLPQLRAASAELEIV
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Genomic sequence for Arabidopsis thaliana BAC F10B6 from chromosome
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana BAC F10B6 from chromosome
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                                                                       complement(join(20954. 21559,21680. .21763,21869. .2202
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Gaps: 0
Percent Identity: 82.353
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   complement(<20954. .>25415)
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Ecker, J.R.
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US-09-485-529-104 x AC005560/rev
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LWLLKSQDSWSEGVVYDEIDLDIEGFPTAVTVAGRDRIYVLYGRVWEGIMGSSYKEEG
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OEKDSKASHDAKELHMFVWSSSASPVSDVFGGGGAGDNVATEQSEGGAKEIRWVVSDQP
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ITRKWQIIVDSLIRIKPIGEMMAIPVINEAMENVVSEIMETYGWICRRIAEVLPNVHS
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FLYHQDRESLMEFGNETDERAREAESRVRELEEEVRKMSDEIKSRIESEEDCLVDSIL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ASFVSKDESISLGRIFLEANSEDKCCETLLRKWDQLKPTTQKFVSLVSWYRREKEK
ECLIMNLAKAEQEVELVSEQNRELDRENRKFLRQCSAERSHGSNKFNKRKSIKMMSSP
IEKRIELSSQEFID"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NVTRVKPAKKSVDLVINGVSMDĪSGLPVPICTCTGAPQQCYRWGCGGWQSACCTTNIS
MHPLPMSTKRRGARISGRKMSQGAFKKVLEKLASDGFNFGNPIDLKSHWARHGTNKFV
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YPEELHLQQPLTPKMVIFWVLFLRIRWWFDKQVCKSSSTTKGDSLVSVGAEGALGFNE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MQSTCVYRECMRNHAAKLGSYAIDGCREYSQPSTGDLCVACGCH
RSYHRRIDVISSPQINHTRFPFTSLRRVKQLARLKWKTAEERNEEEEDDTEETSTEEK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MTVORRRKSKFTAEOREAMKDYAAKLGWTLKDKRALREEIRVFCEGIGVTRYHFKTWV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement(join(17635. .17815,17901. .18019,18141. .18194,
18300. .18406,18547. .18611,18742. .18950))
/note="hypothetical protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IVRPYEVKSLGESFKSLCSPKEGSKVIFGQALKVGTSLTFVGEAVRDKAGNLMIQKSK
EQSLIVFSEESSFDEMVNNMKSQSELCVILAKIFGSIAVAIAVVYGVDYARKVLLPFV
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  11067. .1906
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    complement(13762. .14781)
/note="hypothetical protein"
                                                                                                                                                                                                                                /note-"hypothetical protein"
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                                                                                                                                                                                                                                                                                                                           /evidence=not_experimental/product="F10B6.4"
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                                                                                                                       Department of Biology, University of Pennsylvania, 38th Street and Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA Hamilton Walk, Philadelphia, Pennsylvania 19104-6018, USA 4 (bases 1 to 132699) Arabidary Pannsylvania 19104-6018, USA 5 Cheuk, R., Shinn, P., Brooks, S., Buehler, E., Chao, Q., Chol, C., Khan, S., Kim, C., Altafi, H., Bei, B., Chin, C., Chiou, J., Chol, E., Conn, E., Conn, E., Conn, E., Conn, E., Conn, E., Conn, E., Sakano, H., Enz, C., Li, J., Liu, A., Liu, S., Mukharsky, N., Nguyen, M., Palm, C., Pham, P., Sakano, H., Schwartz, J., Southwick, A., Thaveri, A., Toriumi, M., Vaysberg, M., Yu, G., Davis, R., Federspiel, N., Theologis, A. and Ecker, J. Direct Submission

Submitted (28-JUN-2000) Arabidopsis thaliana Genome Center, Department of Blology, University of Pennsylvania, 38th and Hamilton Walk, Philadelphia, Pa 19104-6018, USA 1.1999 this sequence version replaced gi:4731042.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         complement(join(144. 278,360. 491,576. .673,814. .1435, 1749. .1867,2161. .2310,2441. .2565,2698. .2742,2837. .2902, 2979. .3031,3117. .3234,3314. .3415,3498. .3655,3741. .3818, 3894. .3965,4054. .4104,4138. .4420))
//note="similar to Na/H antiporter dbj|BAA89487.1"
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GTAGGRYLENGTRVPYLVILIVIGIPLGSIGLICILIKLYSSYSISKKILEKYGTKHNL
GTAGGRIGTRINNGINPDIAVELPVLEPSIFSMDVHQIKRCMGQWVLLAGPGVLIST
FCLGALIKLIFPYNWDWTSILLGGLIGATDPVAVVALLKELGASKKWTTLIOCESIA
NDGVSVVVPQLFKKWMGHNSDWGSIIKFLVQNSFGAVGIGLAFGIASVFWLKFIFND
FWAYITANTLYFMSGVIIASSYLSGGTITVWLIGMFPARTAFKGSHQSHHFW
EWAAYITANTLYFMSGVIIASSVLSGGTITVWLGMFPARTAFKGSSHQSHHFW
SWSFLFLIKLYLVQLSRCVVVGVLYPLLCRSGYGLDWKESIILTWSGLRAVLQFLFTG
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GSADWPTVIRHISSLKDLEGRQVNPHDGYERGSLDPTNIMDIRIRELMGISQCVVNS
GCTSVVPKVRIDSRLLPVSGVQAAVEMENLDDGRITQCTANVLMQSVDEALDLVSTSS
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LHIFLGNSNIASTVINESEVEGEBAKQFLEDVRDSFPQVLSVLKTRQVTHYVLNHLNG
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SJOHIG6881. .7029,7140. .7226,7392. .7876,7961. .8180)
/note="similar to transmembrane 9 superfamily member 2
91|4758874: similar to dbj|AV442489.1, 9b|A1996021.1,
emb|F14395.1"
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GPFHNPSETYRYFDLPFCIPEGVKEKKEALGEVLNGDRLVSAPYKLNFRDEKESEVYC
NKKLSKEEVKQFRKAVEKDYYFQMYYDDLPIMGFIGKVDKDIKSDPSEFKYFLYKHIQ
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TQLFTLTIFIFMLALVGVFYPYNRCALFTALVVIYALTSGIAGYTSASFYCOLEGKSW
VRNLLLTGCLFCGPLFLFFCFLNTVAITYTATAAAPFGTIVVIVLNTTVTPLVLG
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RSLAIGETDA"
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         (bases 1 to 132699)
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                                               Ecker, J.R.
Direct Submission
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Location/Qualifiers
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28342. .28470,28565. .28652,28747. .28969)
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similar to EST gb|N96048.1"
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LAFOYASKOLFOFNKLASREKELWKRRTELENLCRAHIEADFISTSLEBRSTALLDSGT
KRLVDPSELLTHINTIKLASREKELINTKRTELENLCRAHIEADFISTSCEBRSTALLDSGT
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AGRGGHVNLKHABRARIITVNKIPSMVDNLIKKTLLMEDETRKSFLYDGVRLVSILEDY
                                                               ELEKECLEIYRRVDEAANSKAQLHOSLVSIEAEIASLLAALGVFNSHSPMKAKEGSK
SLKEKLAAVRPMLEDLRLQKDERMKQFVDIKAQIEKMSGEISGYSDQLNKTWVGSLAL
DEQDLTLRKLNEYQTHLRSLQKEKSDRLNKVLDYVNEVHTLCGVLGVDFGQTVSEVHP
                                                                                                                                                                                                                                  KLTRKQQEEEKRRYRDQKKMQDLLIKRRESIYGSKPSPRRSNSVRKTNGYNGDASVPP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /translation="MTYIYRDTKITTKSTIPFLIFFLECFSNLSMATLKHKPVNLVFY
VYNLIIIFSSHSSTAELRRLLQPSKTDGTVSFLVIGDWGRRGSYNQSQVALQMGEIGE
                                              /translation="MLEIESPISLCFRINTICNALLRELOKIWVDIGESDAEKDRMLM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota Nitidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosidas II; Brassicales; Brassicaceae; Brassica. 1 (bases 1 to 1779)
Renard,M., Delourme,R., Barret,P., Brunel,D., Froger,N. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Mutant gene of the gras family and plants with reduced development
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     containing said mutant gene
Patent: WO 0109356-A 1 08-FEB-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 17
Gaps: 0
Percent Identity: 82.353
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/codon_start=1
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/db_xref="taxon:3708"
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/protein_id="AAF79248.1"
/db_xref="G1:8778239"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AX081276 1779 bp DNA Sequence 1 from Patent WO0109356.
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1. .1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AC006917 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AX081276.1 GI:13170125
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Ratio: 4.118
Percent Similarity: 100.000
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Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: gb_pat:AX081276
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LOCUS AX081276
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SOURCE
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VERSION
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RLRPSSPOSMYTSPSPAGYIGTTYTTYTESTRPLILVDSQDNGYRKUHAHLAACABAV
QSSNLTLAPALVKQIGFLAVSQAGAMRKVATYFAEALARRIYRLSPPOTQIDHSLEDT
LQMMFYETCPYLKFAHFTANOAILEAPEGKKRWHYIDFSMNGCLQMPALMQALALREG
GPPSFRLFGIGPPAADNSDHLHEVGCKLAQLAEAIHYEFEYRGFVANSLADLDASMLE
LRPSETEAVAVNSVPELHKLLGSTGGIEKVFGVVKQIKPVIFTVVEQESNHNGFVELD
RFTESLHYYSTLFDSLEGAESGORVWASEVYLGKQICNLVACCEPDRYERHFTLSQWS
NRFGSSGFAPAHLGSNAFKQASTLLALFNGGEGYRVENNGCLMLSWHTRPLITTSAW
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LQMIFYETCPYLKFAHFTANQAILBEPEGKKRYHVIDFSMNGCLQWPALMQALALREG
GPSFRLTGIGPPAADNSDHLHEVGCKLAQLAEAIHVEFEYRGFVANSLADLDASMLE
LRPSETEATAVNNSVFELHKLLGFTGGIEKTGGIEVFGVYEGVYED
RFTESLHYYSTLFDSLEGAPSSQDKVMSEVYLGKQICNLVACEGPDRVERHETLSQWS
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GYGGKYKSSEMAEVALKLEQLETWHGNAQEDGLAHLATDTYHINPAELYSMLDNML
TELAPPAATTGSNALNPEINNNNGFFTGGDLKAIFGENAVCRRSNOPAFAVDSSSNK
RLKPSSSPDSMYTSPSPAGVIGTTYTTGSTRPLILVDSQDNGVRLVHALMACAEAV
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Renard,M., Delourme,R., Barret,P., Brunel,D., Froger,N. and
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Patent: WO 0109356-A 3 08-FEB-2001;
INSTITUT NATIONAL DE LA RECHERCHE AGRONOMIQUE (INRA) (FR)
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Gaps: 0
Percent Identity: 76.471
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/db_xref="taxon:3708"
60. .1778
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LOCUS AXO81278 1779 bp DNA
DEFINITION Sequence 3 from Patent WO0109356.
ACCESSION AXO81278
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56

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alignment_scores:
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SOURCE
ORGANISM
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ORIGIN
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AUTHORS
TITLE
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JOURNAL
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AUTHORS
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                                                                                                                                                            VERSION
NRFGSSGFAPAHLGSNAFKQASTLLALFNGGEGYRVEKNNGCLMLSWHTRPLITTSAW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Triticum aestivum
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota, Varidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Boenatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae; Triticum.
1 (bases i to 200)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 69 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                            24-AUG-2000
                                                                                                                                                                                                                              7 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 15
Gaps: 0
Percent Identity: 93.333
                                                                                                               0
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                                                                                                                              Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Triticum aestivum"
/db_xref="taxon:4565"
                                                                                                 Length:
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58 c 84 g 27 t
                                                                                                                  Gaps:
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172
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179
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188
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                                                                                                                                                                                                    Align seg 1/1 to: AX081278 from: 1 to: 1779
                                                                                                                                                                                                                                                                                                                                                                                AXUU5860 200 bp DNA
Sequence 69 from Patent WO9909174.
AX005860
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                           475
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                         430 c
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US-09-485-529-104 x AX081278
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US-09-485-529-104 x AX005860
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4.643
93.333
                                                                                                                            Percent Similarity: 100.000
                                                                                                                  .882
             KLSAVH
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LOCUS AX005860
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VERSION
KEYWORDS
SOURCE
ORGANISM
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                         BASE COUNT
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AUTHORS
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                                        ORIGIN
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Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
1 (bases Triticae; Triticum.
1 (bases 1 to 416)
Harberd.N.P. and Peng,J.
Genetic control of plant growth and development
Genetic control of plant growth and development
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Enkaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosladae; eurosids I; Fabales; Fabaceae; Papillonoideae; Dalbergieae; Andira.

1 (bases 1 to 524)

Dutech,C., Ansellem,L., Billotte,N. and Jarne,P.
Characterization of (GA)n microsatellite loci using an enrichment protocol in the neotropical tree species Youacapoua americana Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
Locus Ar224770 524 bp DNA DEFINITION Andira aubletii clone BwA6-II microsatellite sequence.
ACCESSION AF224770
                                                                                                                                                                       24 - AUG - 2000
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Dutech,C., Amsellem,L., Billotte,N. and Jarne,P.
Direct Submission
Submitted (14-3AN-2000) CEFE, CNRS, 1919 route de Mende,
Montpellier cedex 05 34293, France
Location/Qualifiers
Length: 13
Gaps: 0
Percent Identity: 100.000
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/db_xref="taxon:4565"
168 c 129 g 60 t
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/organism="Andira aubletii"
/db_xref="taxon:115636"
                                                                                                                                                        алиозвор 416 bp DNA
Sequence 18 from Patent WO9909174.
AX005809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AX005809 from: 1
                                                                                                                                                                                                                                                  AX005809.1 GI:9928806
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US-09-485-529-104 x AX005809
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Percent Similarity: 100.000
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                                                                                                 seq_name: gb_pat:AX005809
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4987
6131
6231
7449
7549
8848
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
LOCUS AC015886 188716 bp DNA HTG 07-MAY-2001
DEFINITION Mus musculus clone CT7-378P20, WORKING DRAFT SEQUENCE, 26 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus. 1 (bases 1 to 188716)
Birren, B., Linton, E., Nusbaum, C. and Lander, E. Mus musculus chromosome, clone CT7-378P20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (17-NOV-1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 7, 2001 this sequence version replaced gi:7230250.

All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center: Whitehead Institute/ MIT Center for Genome Research
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Center clone name: 378 P.20
------ Summary Statistics
Sequencing vector: M13; M77815; 82% of reads
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
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                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 62.500
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                                                                                                                                               108
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AC015886.4 GI:13959257
HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                     /rpt_unit=ga
90 c
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87.500
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                                                                                                                                            144
                                                                                                                                                                                                                                                                                           Ratio
                                                  repeat_region
                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                          BASE COUNT
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JOURNAL
REFERENCE
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JOURNAL
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AUTHORS
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SOURCE
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Sequencing vector: Plasmid; n/a; 18% of reads
Chemistry: Dye-primer-amersham; 84% of reads
Chemistry: Dye-primer-amersham; 84% of reads
Assembly program: Pitrap; version 0, 960731
Consensus quality: 175387 bases at least Q40
Consensus quality: 181747 bases at least Q20
Consensus quality: 184707 bases at least Q20
Insert size: 173000; agarose-fp
Insert size: 173000; agarose-fp
Quality coverage: 4.8 in Q20 bases.
* NOTE: This is a "working draft' sequence. It currently
* consists of 26 contigs. The true order of the pleces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               9371 10070; gap of 100 bp 11023 bp in length 11324 11423 app of 100 bp 11324 11423 in length 11324 11572; contig of 1153 bp in length 11324 12572; contig of 1149 bp in length 12573 12672; gap of 100 bp 12573 12673; gap of 100 bp 14268 15746; contig of 1495 bp in length 14168 14267; gap of 100 bp 15747 15846; gap of 100 bp 15747 17516; gap of 100 bp 17417 17516; gap of 100 bp 17517 18799; contig of 1570 bp in length 17517 18799; contig of 1243 bp in length 18900 20317; contig of 1418 bp in length 18900 20317; contig of 1418 bp in length 20318 20478; gap of 100 bp 20418 22567; gap of 100 bp 20550 bp in length 22568 22567; gap of 100 bp 22558 22567; gap of 100 bp 22558 22550; contig of 2353 bp in length 22558 22550; contig of 2353 bp in length 22558 22550; contig of 2353 bp in length 22558 2550; contig of 2353 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     1021 1120: gap of 100 bp 1121 2393: contig of 1273 bp in length 2394 2494 3639: contig of 1146 bp in length 3640 3739: gap of 100 bp 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            44639; gap of 100 bp 55525; gap of 16554 bp in length
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118724 151284: contig of 32561 bp in length
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44539: contig of 10091 bp in length
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151385 188716: conti
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8847: cor
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Page 28

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2502 others
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ORIGIN
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Align seg 1/1 to reverse of: AC015886 from: 1 to: 188716

seq_name: gb_pr:AL355796

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Uniect Submission

Uniect Submission

Uniect Submission

CBIO 1SA, UK. E-mail enquiries: humquery@sanger.ac.uk Clone

requests: clonerequest@sanger.ac.uk

On Dec 24, 2000 this sequence version replaced gi:11990033.

During sequence assembly data is compared from overlapping clones.

Where differences are found these are annotated as variations together with a note of the overlapping clone name. Note that the variation annotation may not be found in the sequence submission corresponding to the overlapping clone, as we submit sequences with only a small overlap as described above.

This sequence has been finished according to sequence map criteria as follows. An attempt is made to resolve all sequencing problems, such as compressions and repeats, but not necessarily within known annotated repeat sequence elements. Where the sequence is ambiguous, there is an annotation using the 'unsure' feature key. The following abbreviations are used to associate primary accession numbers given in the feature table with their source databases:

Em:, EMBL; Sw:, SWISSPROT; Tr:, TREMBL; Wp:, WORMPEP; Information on the WORMPEP database can be found at http://www.sanger.ac.uk/Projects/C_elegans/wormpep This sequence butter information contigs of human contracts of constructed by the Sanger Centre Chromosome 6 Mapping chromosome 6 Constructed by the Sanger Centre Chromosome 6 Mapping
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 IMPORTANT: This sequence is not the entire insert of clone RP11-46B11 It may be shorter because we sequence overlapping sections only once, except for a 100 base overlap. The true left end of clone RP11-46B11 is at 1 in this sequence. The true left end of clone RP3-50BD13 is at 151987 in this sequence. The true right end of clone RP11-454P17 is at 95829 in this
seq_documentation_block:
LOCUS AL355796 152086 bp DNA PRI 23-DEC-2000
DEFINITION Human DNA sequence from clone RP11-46B11 on chromosome 6, complete
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Group. Further information can be found at http://www.sanger.ac.uk/HGP/Chr6 RPI1-46B11 is from the library RPCI-11.1 constructed by the group of Pieter de Jong. For further details see
                                                                                                                                                                                                                                                                                      Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 152086)
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7689. .7939
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1194. .1456
/note="ilpA7 repeat: matches 5881. .6143 of consensus"
1457. .2384
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/note="LlPBa repeat: matches -235. .1639 of consensus"
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VECTOR: pBACe3.6
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1. .152086
/organism="Homo sapiens"
/db_xref="taxon:9606"
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/clone="RP11-46B11"
/clone_lib="RPCI-11.1"
                                                                                                                                           AL355796
AL355796.11 GI:11991379
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Direct Submission
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                                                                                                         sequence.
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On 9.22... y800

On 7.22... y800

Note="Lil repeat: matches 2157...2706 of consensus" 10305...11076... inches 11396

Anote="Lil Phb repeat: matches 5432...6143 of consensus" 12975...1396

Anote="Lil repeat: matches 2310...2707 of consensus" 13649...13876

Anote="Lil repeat: matches 3560...3775 of consensus" 15684... 15899

Anote="Lil repeat: matches 3560...3775 of consensus" 16763...1868

Anote="Lil repeat: matches 4359...4985 of consensus" 18763...18951

Anote="Lil Repeat: matches 4359...4985 of consensus" 18763...18951

Anote="Lil Repeat: matches 72...262 of consensus" 18763...18953

Anote="Min repeat: matches 64...151 of consensus" 18763...18953

Anote="Min repeat: matches 64...151 of consensus" 18399...2303... 18309

Anote="Min repeat: matches 158...228 of consensus" 18399... 23039... 18099... 13099

Anote="Min repeat: matches 1...1300 of consensus" 18399... 13005... 13005

Anote="Min repeat: matches 1...1300 of consensus" 18309... 13005... 13005

Anote="Min repeat: matches 1...1300 of consensus" 18309... 13009... 13009

Anote="Min repeat: matches 1...1300 of consensus" 18309... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13009... 13000... 13009... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 13000... 1
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41372. 41526
/note="MIR repeat: matches 23. .188 of consensus"
41546. 42004
/note="MLTIC repeat: matches 1. .464 of consensus"
43170. 4358
/note="Limble repeat: matches 4169. .4555 of consensus"
43559. 43682
/note="Limble repeat: matches 6032. .6155 of consensus"
43683. 43860
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45567. .45626

//note="LinkBz repeat: matches 5779. .5108 of consensus"

45627. .45909

//note="LinkBz repeat: matches 6. .289 of consensus"

45910. .46205

//note="LinkBz repeat: matches 5107. .5400 of consensus"

46607. .47209

//note="TigGER1 repeat: matches 1800. .2418 of consensus"
                                                                                                                                                                                                                                 47210. 47564
/note="L1MBB repeat: matches 5789. .6147 of consensus"
47565. 47938
/hote="MWTD repeat: matches 1. .394 of consensus"
47939. 48009
/note="L1MB2 repeat: matches 4555. .4731 of consensus" 43861. .44169
/note="Alux repeat: matches 1. .309 of consensus"
                                                             /note="L1MB2 repeat: matches 4731. .5779 of consensus"
45223. .45566
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49939. .50006
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                                                                                          /note="MER44A repeat: matches 1. .333 of consensus"
45567. .45626
                                                                                                                                                                                                                                                                                                                                            /note="MIR repeat: matches 3. .68 of consensus" 2007. .50317 /note="AluSx repeat: matches 1. .312 of consensus" 50318. .50406
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Gaps: 0
Percent Identity: 56.250
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US-09-485-529-104 x AL355796/rev
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60683.
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3.200
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Oncomparison of the property o
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                                                                                                                                                                                                                                            Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Buteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 179481)
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**Estimated insert size: 179221 - sum-of-contigs
Quality coverage: agrose-FP - N/A
Quality coverage: 9.4 x in Q20 bases; sum-of-contigs estimation
      DNA HTG 13-JUL-2003
14 clone RP23-46517 strain C57BL6/J,
14 unordered pieces.
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Contact: htgs@sequence.aecom.yu.edu
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Chemistry: Dye-terminator Big Dye; 100%
*Consensus quality: 177183 at least Q20
*Consensus quality: 17458 at least Q30
*Consensus quality: 174495 at least Q30
Estimated insert size: agarose-FP - N/A
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                                                                                                                                                       HTG; HTGS_PHASE1; HTGS_DRAFT.
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                                                                                                                       AC034100.8 GI:14717146
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122767
122787
151382
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174509
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      LOCUS
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JOURNAL
REFERENCE
AUTHORS
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JOURNAL
                                                                                              ACCESSION
                                                                                                                                                                                                                                                                                                           REFERENCE
                                                                                                                          VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /protein_id="AaD43151.1"
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FIQLVLDLAISVVKFLFVPILAVSSISEMSYCAHERKLALVPFPLVIGWVAGVLQET
ALKISPRLKEAEVFWHLIAMMMFFTLIKLPGPYYPYWGRLLVPHFANGVLLRALWSMF
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                PPPPVYSPPPPTFSPPPTHNTNQPPMCAPTPTQAPTPSSETTQVPTPSSESDQSQ1LS
PVQAPTPVQSSTPSSEPTQVPTPSSSESYQAPNLSPVQAPTPSSETSQVPTP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            SSESNQSPSQAPTPILEPVHAPTPNSKPVQSPTPSSEPVSSPEQSEEVEAPEPTPVNP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /translation="MQMDSAQNQFNKRARLFEDPELKDAKVIYPSNPESTEPVNKGYG
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(9112764114), 114G10T7 (9112597578), and 114G1HT7
(9112597579)"
                               Location of ests VBVQD12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Join(28449, .28680,28766, .28965,29065, .29313)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: AC007504 from: 1 to: 125021
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Hypothetical Protein"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
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                               /note="Unknown Protein; Lo
(gi|757594 and gi|757593)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /protein_id="AAD43153.1"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23803. .26346
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23803. .26346
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                                                                                                                                                                                                                                                                                                                                       21730, .21921
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21730, .21921
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /gene="F13F21.8"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /codon_start=1
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contig of 202 bp in length gap of unknown length contig of 199 bp in length

177244:

177045:

176824 177026 177046

seq_name: gb_htg:AC034100 seq_documentation_block:

alignment_scores

alignment_block:

177025

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Mesorhizobium lot1
                                                                                                                                                                                                                                         Kaneko, T.
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   ORGANISM
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AUTHORS
TITLE
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LOCUS AP002997 329709 bp DNA BCT 15-1
BCT 15-1
BCT 15-1
BCSETNITION MESOTALSOBIUM 10t1 DNA, complete genome, section 4/21
ACCESSION AP002997, 2 GI:14022051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              415 others
177264: gap of unknown length
178663: contig of 1399 bp in length
178683: gap of unknown length
179208: contig of 525 bp in length
179228: gap of unknown length
179481: contig of 253 bp in length.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                        Vector_side.left"
168088. .174488
/note="assembly_name:Contig93"
174509. .175363.
/note="assembly_name:Contig92"
175384. .175665.
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50783. .92572
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92593. .122766
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122787. .151381
                                                                                                                                                                                                                                                                                                                                                                                             vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Length:
                                                                                                                       1. .179481
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                                                                                                   Location/Qualifiers
1. .179481
                                                                                                                                                                                                       /clone="RP23-46517"
                                                                                                                                                                                                                                                                                                                                                                               clone_end:SP6
                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:T7
                                                                                                                                                                                                                           /sex="male"
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US-09-485-529-104 x AC034100
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3.917
85.714
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                              178664
178684
179209
179229
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                                                                                                                       source
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. Mesorhizobium loti (strain:MAFF303099) DNA.

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MRTFSYVLAKGEPK ITITOTOVRAALOLARAALIXAGTKLLIMEKONTEHVDRIHFRAAF
GSFIDPKYAAVLGIIPDCDLDKVSAVGNAGARAALINRGYRREIEETVOS
TALEPKFQEHFVYAMALPNKVDPFPKLSAAVKLPPRKTVSEDGIAGDATPRRRSREGH
                                                                                 Kaneko, T., Nakamura, Y., Sato, S., Asamizu, E., Kato, T., Sasamoto, S., Watanabe, A., Idesawa, K., Ishikawa, A., Kawashima, K., Kimura, T., Kishida, Y., Kiyokawa, C., Kohara, M., Matsumoto, M., Matsuno, A., Mochizuki, Y., Nakayama, S., Nakazaki, N., Shimpo, S., Sugimoto, M., Takeuchi, C., Yamada, M. and Tabata, S. Complete genome structure of the nitrogen-fixing symbiotic bacterium Mesorhizoblum loti
Bacteria; Proteobacteria; alpha subdivision; Rhizobiaceae group;
Phyllobacteriaceae; Mesorhizobium.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (05-DEC-2000) Takakazu Kaneko, Kazusa DNA Research Institute, The First Laboratory for Plant Gene Research; Yana 1532-3, Kisarazu, Chiba 292-0812, Japan (E-mail: Kaneko@kazusa.or.jp, Thizobase/, Tal: http://www.kazusa.or.jp/rhizobase/, Tel: 81-438-52-3935 (ex.2338), Fax: 81-438-52-3934)
On May 11, 2001 this sequence version replaced g1:11994965.
Location/Qualifiers
1. 329709
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CDS

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 KSYGADGIVVRNDIKTVADLKGKNVASSAPGTSPYFLLAWVLNKNGMSTKDVTVVNLE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      DGPNNQGAPVNLTRDGVVRQGIVINGLPLMTRGGLSGAYDVNDLDRYYSDCVIGGPGA
FMIPVNDWTQFPEAIRRKLVLELAGPASPQWAAEEADHPPVVLTQDKPAADCQIGEKM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           24-AUG-2000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to reverse of: AP002997 from: 1 to: 329709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 16
Gaps: 0
Percent Identity: 62.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /note="hypothetical protein"
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LOCUS AX005855 309 bp DNA
DEFINITION Sequence 64 from Patent WO9909174.
ACCESSION AX005855
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  complement(10906. .13467)
                                                                                                   Ltable=11
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87.500
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KEYWORDS
CDS
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5113. .5379
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FAWLREEYNRGVAVGGLCTGAHILAAAGLLSNKRCAIHWENLPGFSEAFPKANVFADL
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CDS

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DFGSTILDSVASNY I DSKA EYENSTNLAASYNTQDI QVKQQEFDPSEASEPI DI GNTK
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                                                                                                                                 Andersson.A.G.E.
Direct Submission
Submitted (11-NOV-1998) S.G.E. Andersson,
Siv.Andersson@molbio.uu.se, Dept. of Molecular Biology, University
of Uppsala, Husargatan 3, Uppsala, S.751 24, SWEDEN
ON NOV 13, 1998 this sequence version replaced 91:3860788.
      The genome sequence of Rickettsia prowazekii and the origin of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /product="TAIL-SPECIFIC PROTEASE PRECURSOR (ctp)" /protein_id="CAA14691.1"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /codon_start=1
/transl_table=11
/product="DNA GYRASE SUBUNIT B (gyrB1)"

    .312430
    /organism="Rickettsia prowazekii"
/strain="Madrid E"

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/db_xref="GI:3860789"
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                                                                     Nature 396 (6707), 133-140 (1998)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="taxon:782"
76. .1830
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2025. .4013
/gene="RP227"
2025. .4013
                                                                                                                                                                                                                                                                                                                                                                                  Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product-"unknown"
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/transl_table=11
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/gene="RP228"
4122. .5447
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/gene="RP227"
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/gene="RP228"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /gene="RP226"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /gene="RP226"
76. .1830
                                         mitochondria
                                                                                                        99039499
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JOURNAL
                                                                                                                                        REFERENCE
AUTHORS
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          TITLE
                                                                                                                                                                                                                                                                                                                                               COMMENT
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooldeae; Triticae; 
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
LOCUS RPXX02 312430 bp DNA BCT 12-NOV-1998
DEFINITION Rickettsia prowazekii strain Madrid E, complete genome; segment
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AJ235271. GI:3868717
Complete genome.
Rickettsia prowazekii.
Rickettsia prowazekii.
Rickettsia prowazekii.
Rickettsia prowazekii.
I (bases 1 to 312430)
Andersson, S.G., Zomorodipour, A., Andersson, J.O.,
Sicheritz-Ponten, T., Alsmark, U.C., Podowski, R.M., Naslund, A.K.,
Eriksson, A.S., Winkler, H.H. and Kurland, C.G.
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                                                                                                                                                                                                                                                                                                                                            /organism="Triticum aestivum"
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102 c 102 g 45 t
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95
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                                                                                                                                                                                                                                                                                                                                                                               /db_xref="taxon:4565"
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US-09-485-529-104 x AX005855
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Percent Similarity: 100.000
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ORIGIN
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JOURNAL
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SOURCE
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                                                                                                                                        AUTHORS
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                                                                                                            REFERENCE
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gene

CDS

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/translation="MKTYSARPSEIEKKWWVIDAKNVVLGRLASRVAIMLRGKHKPSF
TPHLDGGDNIIIINAEHIKLTGKKLNPKDGKVYYRHTGFPGGIKDTTAGKILSGKYPE
RVIKNAVKRHITRNVLGAKOMSNLYVYANCEHPHMAQOPTIVDFASENPKNKK"
10753. 11238
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /translation="mrnssnkylddpyrpgygmmilnadnqifygkridfkisswqmp
QGGIVPGETPSIAAMREMLEEIGSNKGYIIAESKCWYSYDVPSFLIPKLWNGNFRGQK
QRWFLIRFTGNNKDINIHTSNPEFDQWRWTSLDELLSIIIPFKRKLYQAVVKEFESLI
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Molecular cloning of the full-length cDNA of (S)-hydroxynitrile
lyase from Hevea brasiliensis. Functional expression in Escherichia
                                                                                                                                                                                                                                               /product-"30S RIBOSOMAL PROTEIN S9 (rps!)"
/protein_id="CAA14697.1"
/db_xref="G1:3860797"
/translation="MTELKIKTEKVVKOLTKESLKSVLKIPKEKIDSVSKFYATGKRK
                                                                                                                                                                                                                                                                                                                                                    NAIARVWLKVGKGKIVVNNKILNQYFPSETYVKTILLQPFILTKTIDQYDVICTVKGGG
ISGQKGAILHGISKALDKSAPCFHAILRKGGLLTRDSRVVERKKYGQRKARKKTQFSK
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Hevea brasiliensis
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae: eurosids I; Malpighiales; Euphorbiaceae; Hevea.

1 (bases I to 1078)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            13-MAR-1996
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/protein_id="CAA14698.1"
/db_xref="GI:3860798"
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Gaps: 0
Percent Identity: 60.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /gene="tRNA Met (CAT)"
complement(12284. .12769)
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/gene="tRNA Met (CAT)"
11279. .11352
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/product="unknown"
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                                                                                                                       /gene="RP234"
10753. .11238
/gene="RP234"
/codon_start=1
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US-09-485-529-104 x RPXX02
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1 191 c 339 g 324 t
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( bases 1 to 1091)

Hasslacher, M., Schall, M., Schab, H., Hayn, E.M., Kohlwein, S. and
coli and Saccharomyces cerevisiae and identification of an active
                                                                  2 (bases 1 to 1078)
Hasslacher, M., Schall, M., Hayn, M., Griengl, H., Kohlwein, S.D. and
                                                                                                                                      Submitted (09-NOV-1995) Meinhard Hasslacher, Department of Biochemistry, University of Technology Graz, Petersgasse 12/2, Graz, 8010, Austria, 8020 Location/Qualifiers
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Musmalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mussae; I to 161592)

El (bases I to 161592)

Metzker, M.L., Lewis, L.R., Hume, J., Edwards, C., Garner T., Dederich, D., Thomas, S., Okwonu, G., Carlock, C., Garner T., Addison, S., Pace, A., Williams, G., Bonnin, D., Brooks, A., Brown, J., Buhay, C., Davis, C., Delgado, O., Ding, Y., Dugan-Rocha, S., Fernandez, C., Ferraguto, D., Forcum-Tansey, J., Gill, R., Gorrell, J.H., Gunaratne, P., Haller, G., Hernandez, J., Hogues, M., Hosak, H., Hou, X., Huber, J., Jackson, L., Jia, Y., Kelly, J., Kelly, S., Kovar, C., Liu, W., Loulseged, H., Lozado, R.J., Martin, R., Massey, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Nasye, E., McLeod, M.P., Mei, G., Moore, S., Morgan, M., Morris, S., Muzny, D.M., Rives, M., Scherer, S., Sodergren, E., Weinstock, G., Morley, K. and Gibbs, R.

Unpublished
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On Nov 4, 2000 this sequence version replaced gi:8248608.

Center: Baylor College of Medicine
Center: Baylor College of Medicine
Center: Baylor College of Medicine
Genter code: BCM
Web site: http://www.hgsc.bcm.tmc.edu/
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Direct Submission
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                                              (see http://www.hgsc.bcm.tmc.edu/docs/Genbank_draft_data.html).
NOTE: This is a "working draft' sequence. It currently consists of 64 contigs. The true order of the pieces is not known and their order in this sequence record is arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will be preserved.
            Quality coverage: 0x in Q20 bases; agarose-fp estimation Quality coverage: 1.8x in Q20 bases; sum-of-contigs estimation
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       18823. .26781
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 26882. .43389
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                              gap of unk contig of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /db_xref="taxon:10116"
/clone="RP31-494C9"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         'strain="Brown Norway
                                                                                                                                                                                                                                                                                                       26881: gap of
                                                                                                                                                                                                                                                                                                                                                                                         gap of
                                                                                                                                gap of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           vector_side:right"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_lib="RP31"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            172670. .214605
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    clone_end:T7
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US-09-485-529-104 x AC091618/rev
                                                                                                                                                                                            12572:
12672:
18722:
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26781:
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6749:
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3.750
92.308
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129940
130040
172570
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3124
6650
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12573
12673
18723
18823
26782
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43490
67366
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Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Ayele,K., Beckstrom Sternberg,S.M., Benjamin,B., Blakesley,R.W., Ayele,K., Beckstrom Sternberg,S.M., Benjamin,B., Blakesley,R.W., Bouffard,G.G., Brinkley,C., Brooks,S., Dietrich,N.L., Granite,S., Gupta,J., Ho,S.-L., Idod,J.R., Karlins,E., Lee-Lin,S.-Q., Legaspi,R., Lim,M., Maduro,Q.L., Maduro,V.B., Masiello,C., Mastrian,S.D., McCloskey,J.C., McDowell,J., Pearson,R., Prasad,A., Shevchenko,Y., Snyder,B., Stantripop,S., Thomas,J.W., Thomas,P.J., Tiongson,E.E., Touchman,J.W., Tsurgeon,C., Vogt,J.L., Walker,M.A., Wetherby,K.D., Zhang,L.H. and Green,E.D.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Norway rat.
Rattus norvegicus
Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
LOCUS AC091618 214605 bp DNA
DEFINITION Rattus norvegicus clone RP31-494C9 strain Brown Norway, WORKING
DRAFT SEQUENCE, 11 unordered pieces.
ACCESSION AC091618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Submitted (10-MAY-2001) NIH Intramural Sequencing Center, 8717 Grovemont Circle, Gaithersburg, MD 20877, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequencing vector: plasmid: 100% of reads
Sequencing vector: plasmid: n/a: 100% of reads
Sequencing vector: plasmid: n/a: 100% of reads
Assembly program: Phrap: version 0.990319
Consensus quality: 209557 bases at least Q40
Consensus quality: 211114 bases at least Q20
Consensus quality: 211652 bases at least Q20
Insert size: 188000: agarose-fp
Insert size: 213605; sum-of-contigs
Quality coverage: 7.31x in Q20 bases; sum-of-contigs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NOTE: This is a 'working draft' sequence. It currently consists of 11 contigs. The true order of the pieces is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  is not known and their order in the contigs are represented as arbitrary. Gaps between the contigs are represented as
                                            6390 others
                                                                                                                                                                                                                                                                                                                                                                       Center: NIH Intramural Sequencing Center Center code: NISC
Web site: http://www.nisc.nih.gov
Centact: nisc_mouse@nhgri.nih.gov
Center project Information
Center project name: cgo
Center clone name: 494009
                                                                                                                                                                                                                                                                                                                                                 1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                              Percent Identity: 60.000
                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AC026377 from: 1 to: 161592
                      /clone="RP23-267J8"
40073 a 36398 c 37212 g 41519 t
                                                                                                                                                                             Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AC091618.1 GI:14017490
HTG; HTGS_PHASE1; HTGS_DRAFT.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (bases 1 to 214605)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Direct Submission
                                                                                                                                                    45.00
3.462
86.667
                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x AC026377
                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_htg:AC091618
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Green, E.D.
                                                                                                                                                      Quality:
Ratio:
                                                                                                                                                                                          Percent Similarity:
                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
                                            BASE COUNT
ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TITLE
JOURNAL
REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TITLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VERSION
KEYWORDS
SOURCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               REFERENCE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AUTHORS
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COMMENT

1027 others

DEFINITION

ACCESSION KEYWORDS SOURCE

VERSION

ORGANISM

AUTHORS TITLE JOURNAL REFERENCE AUTHORS

REFERENCE

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* 36323 36986: contig of 664 bp in length

* 36987 37086: gap of 100 bp

* 37087 37086: gap of 100 bp

* 37767 37866: gap of 100 bp

* 37767 37866: gap of 100 bp

* 44314 44413: contig of 6447 bp in length

44414 50170: contig of 5757 bp in length

50171 50270: gap of 100 bp

50171 54190: contig of 3920 bp in length

54191 54290: gap of 100 bp
                                                                                                                                                                                                                                                                                                                                                                                                                          94582 94681: gap of 100 bp 94682 135705: contig of 41024 bp in length 135706 135805: gap of 100 bp 175324: gap of 100 bp 175424: gap of 100 bp 175425 228201: contig of 52777 bp in length.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1100 others
                                                                                                                                                                                                                                                                                                                                                                        191: gap of 100 bp
94581: contig of 35590 bp in length
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 228201
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="RPCI-23 Female Mouse BAC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
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86.667 Percent Identity: 66.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    vector_side:right"
52016 c 52776 g 62491 t
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/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            37087. 37766 /note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           44414. .50170 /
/note="assembly_fragment"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /note="assembly_fragment"
54291. .58891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note="assembly_fragment"
94682, .135705
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /note="assembly_fragment"
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/note="assembly_fragment"
36323. .36986
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /note="assembly_fragment"
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/note="assembly_fragment
clone_end:SP6
vector_side:left"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /organism="Mus musculus"
/db_xref="taxon:10090"
/clone="RP23-2M16"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
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US-09-485-529-104 x AC016814/rev
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58992 94
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             FEATURES
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Birren, B., Linton, L., Nusbaum, C., Lander, E., Allen, N., Anderson, M., Baldwin, J., Barna, N., Beckerly, R., Boguslavkiy, L., Boukhgalter, B., Brown, A., Castle, A., Collangelo, M., Collins, S., Collymore, A., Cooke, P., DeArellano, K., Dewar, K., Domino, M., Donelan, L., Doyle, M., Ferreira, P., FitzHugh, W., Forrest, C., Funke, R., Gage, D., Galagan, J., Gardyna, S., Grant, G., Hagos, B., Heaford, A., Horton, L., Howland, J.C., Johnson, R., Jones, C., Kann, L., Marquis, N., Lehoczky, J., Lieu, C., Locke, K., Macdonald, P., Marquis, N., McEwan, P., McGurk, A., McKernan, K., McLaughlin, J., Meldrin, J., Merrow, J., Naylor, J., Norman, C.H., O'Connor, T., O'Donnell, P., Peterson, K., Pollara, V., Riley, R., Koy, A., Santos, R., Severy, P., Stange-Thomann, N., Stojanovic, N., Subramanian, A., Talamas, J., Wyman, D., Ye, W.J., Zimmer, A. and Zody, M.
                                                                                                                                                                                           AC016814 228201 bp DNA HTG 13-MAY-2001
Mus musculus clone RP23-2M16, WORKING DRAFT SEQUENCE, 12 unordered
                                                                                                                                                                                                                                                                                                                                                                                                                             Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Rodentia; Sciurognathi; Muridae; Murinae; Mus.
1 (bases 1 to 228201)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted March 1999) Whitehead Institute/MIT Center for Genome Research, 320 Charles Street, Cambridge, MA 02141, USA On May 13, 2001 this sequence version replaced gi:12061489.
All repeats were identified using RepeatMasker:
Smit, A.F.A. & Green, P. (1996-1997)
http://ftp.genome.washington.edu/RM/RepeatMasker.html
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ------ Genome Center
Center: Whitehead Institute/ MIT Center for Genome Research
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Center project name: L1541

Center clone name: 2_M_16

Center clone name: 2_M_16

Center clone name: 2_M_16

Sequencing vector: M13; M77815; 16% of reads
Sequencing vector: M13; M77815; 16% of reads
Sequencing vector: Plasmid; m74; 84% of reads
Sequencing vector: Plasmid; m74; 84% of reads
Chemistry: Dye-terminator B1g Dye; 100% of reads
Assembly program: Phrap; version 0.960731

Consensus quality: 224356 bases at least 040
Consensus quality: 22619 bases at least 030
Consensus quality: 226246 bases at least 020
Insert size: 217100; agarose-fp
Insert size: 227101; sum-of-contigs
Quality coverage: 20.7 in 020 bases; agarose-fp
quality coverage: 20.7 in p20 bases; agarose-fp
consists of 12 contigs. The true order of the pieces
* is not known and their order in this sequence record is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           arbitrary. Gaps between the contigs are represented as runs of N, but the exact sizes of the gaps are unknown. This record will be updated with the finished sequence as soon as it is available and the accession number will
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Center code: WIBR
Web site: http://www-seq.wi.mit.edu
Contact: sequence_submissions@genome.wi.mit.edu
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LOCUS AC020887 271519 bp DNA HTG 29-MAR-2000
DEFINITION MUS musculus clone RP23-472H3, WORKING DRAFT SEQUENCE, 86 unordered
                                                                                                                                                                                                                                           Direct Submission

Submitted (10-3M-2000) Production Sequencing Facility, DOE Joint Genome Institute, 2800 Mitchell Drive, Walnut Creek, CA 94598, USA ON Mar 29, 2000 this sequence version replaced gi:6686421.

------Genome Center
Center: Joint Genome Institute
Center: Joint Genome Institute
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-----Summary Statistics
Consensus quality: 168487 bases at least Q40
Consensus quality: 2137951 bases at least Q30
Consensus quality: 213703 bases at least Q20
Estimated insert size: 271519; sum-of-configs estimation
Estimated insert size: 255000; pulse field gel estimation
Quality coverage: 3.65 in Q20 bases; pulse field gel estimation
Quality coverage: 2.84x in Q20 bases; sum-of-contigs estimation
                                                                                                                                     Craniata; Vertebrata; Euteleostomi;
Sciurognathi; Muridae; Murinae; Mus
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Sequencing of Mouse
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alignment_scores:
Quality: 45.00 Length: 15
Ratio: 3.462 Gaps: 0
Percent Similarity: 86.667 Percent Identity: 60.000
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1 AspGluLeuLeualaalaLeuGlyTyrLysValargalaSerAsp 15 ||||||||::||||||||| ||| :::::|||||||||::: |126324 GATGAAGTGCTTGCTGCATGTGGGCTGGAGCTCAGAAGCCTCAGAA 126280

seq_name: gb_htg:AC070284

ation_block: AC070284 Glardia intestinalis clone EJ6500 strain WB-C6, LOW-PASS SEQUENCE SAMPLING. AC070284. AC070284. AC070284. Glardia intestinalis. Glardia intestinalis. Glardia intestinalis Eukaryota; Diplomonadida; Hexamitidae; Glardiinae; Glardia. 1 (bases 1 to 878) Morrison,H.G., McArthur,A.G., Nixon,J., Eakin,N.Q., Kim,U., Crocker,M.C., Hinkle,G., Holder,M.E. and Sogin,M.L. Glardia: a model for ancient eukaryotic genome analysis	Unpublished (Lases 1 to 878) Eakin, N.Q., Morrison, H.G., McArthur, A.G., Nixon, J., Kim, U., Eakin, N.Q., Morrison, H.G., McArthur, A.G., Nixon, J., Kim, U., Crocker, M.C., Hinkle, G., Holder, M.E. and Sogin, M.L. Direct, Submission Submitted (06-JUN-2000) Josephine Bay Paul Center for Comparative Molecular Biology and Evolution, Marine Biological Laboratory, 7 MBL Street, Woods Hole, MA 02543-1015, USA * NoTE: This record contains 1 individual * sequencing reads that have not been assembled into * contiggs. Runs of N are used to separate the reads * and the order in which they appear is completely * arbitrary. Low-pass sequence sampling is useful for	* overlap relationships among clones to be deduced. * However, it should not be assumed that this clone * will be sequenced to completion. In the event that * the record is updated, the accession number will * be preserved. * Docation/Qualifiers 1. 878 /organism="Glardia intestinalis" /strain="Wab-c6" /db_xref="taxon:5741"	, a	x AC070284 AC070284 from: 1 to: 878 LeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16	AAGCTGCGCGCTTCGATTGGATTCAAGATTTATGCGACACATCTT 843 pr:AF090137 ation_block: AF090137 1241 bp mRNA PRI 12-MAR-1999 Homo sapiens carbohydrate sulfotransferase 1 (CHST1) mRNA, complete cds. AF090137 GI:4406151 human.	Homo sapiens Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1241) Li,X. and Tedder,T.F.
int .	JOURNAL U REFERENCE 2 AUTHORS C TITLE S JOURNAL M COMMENT **	FEATURES source	BASE COUNT 235 ORIGIN alignment_scores: Quality: Ratio: Percent Similarity: alignment_block:	o w	regioname: gb_pr:AF090137 seq_documentation_block: LOCUS AF090137 DEFINITION Homo sapiens ACCESSION AF090137 VERSION AF090137 KEYWORDS SOURCE human.	ORGANISM H E E M REFERENCE 1 AUTHORS I

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Bacillus subtilis.
Bacillus subtilis.
Bacillus subtilis
Bacteria. Firmicutes; Bacillus/Clostridium group;
Bacillus/Faphylococcus group; Bacillus.
1 (bases 1 to 2096)
Marasco,R., Varcamonti,M., Ricca,E. and Sacco,M.
A new Bacillus subtilis gene with homology to Escherichia coli progene 183 (1-2), 149-152 (1996)
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Submitted (06-JUN-1996) M. Sacco, Istituto Internazionale di
Genetica e Biofisica, via Marconi 10, 80125, Napoli ITALY
Location/Qualifiers
                                                                                                                                                                               /product-'keratan sulphate
6-sulfo-transferase'
'R 1237. .1458.
Location/Qualifiers
(C12N15/09,C12R1:19);
strandedness: Single;
tropology: Linear;
hypothetical: No;
anti-sense: No;
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    organism="Bacillus subtilis"

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/organism="Homo sapiens"
/db_xref="taxon:9606"
a 526 c 421 g 257
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/protein_id="CAA66987.1"
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/gene="orfRM1"
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FTFGGKSPADARNAMGASRDLLRSLYDCDLYFLEBNIKPPYNHTYDRIFRRGASRYL
CSRPVCDPPGPADLVLEEGDCVRKCGLLNLTVAABACRERSHVAIKTVRYPEVNDLRA
LVEDPRLNLKYIQLYRPROTILASRSFTFRDTYRLRRLWYGTGRKPYNLDVTGLTTVC
EDFSNSVSTGLMRPPWLKGKYMLVRYEDLARNPMKKTEEIYGFLGIPLDSHVARWION
NTRGDPTGRIKYGTYRNSAATAEKWRFRLSYDIVAFAQNACQOVLAQLGYKIAASEE
BLKNDSVSLVERDRFFSFS
197 t
                                                                          91100500
2 (bases 1 to 1241)
L1,X. and Tedder,T.F.
Direct Submission
Submitted (03-SEP-1998) Immunology, Duke University Medical Center,
Durham, NC 27770, USA
                                                                                                                                                                                                                                                                                                                                                                                           /translation="MQCSWKAVLLLALASIAIQYTAIRTFTAKSFHTCPGLAEAGLAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi; Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo. 1 (bases 1 to 1458)
Fukuda,M. and Hanebuchi,N.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EGRAPIAN SUCRATE 6-SULFOTRANSFERASE AND DNA CODING FOR THE SAME PATENT: JP 1998155488-A 1 16-JUN-1998; SEIRAGARU KOGYO CO LTD
OS HOMO Sapiens (human)
PN 1998155488-A/1
PD 16-JUN-1998
PF 29-NOV-1996 JP 1996320535
PI FUKUDA MASAKAZU, HANEBUCHI NAGAMOTO
PC C12N15/09.CO7H21/04,CO7K14/47,C08B37/00,C12N9/10, PC C12P19/26//C12P21/02,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   28-JUL-1999
 CHST1 and CHST2 sulfotransferases expressed by human vascular endothelial cells: cDNA cloning, expression, and chromosomal
                                                                                                                                                                                                                                                                                                                                   /product-"carbohydrate sulfotransferase 1"
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                                                                                                                                                                                                                                  /tissue_type="umbilical vein endothelium"
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Percent Identity: 57.143
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    .1241
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    /db_xref="taxon:9606"

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99168906
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5. 1240
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RFTQGKSPADRRVMLGASRDLLRSLYDCDLYFLENYIKPPPVNHTTDRIFRRGASRVL
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TITLE
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Peng, T., Tabas, I. and Williams, K.J.
Direct Submission
Submitted (30-JUL-1996) Medicine, Thomas Jefferson University, 1020
Locust Street, Philadelphia, PA 19107-6799, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /note="part of the sequence corresponds to an EST, GenBank Accession Number R16177, which is similar to the chicken chondroitin-6-sulfotransferase cDNA sequence, GenBank Accession Number D49915"
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RLCEESPTFAYNLSRKTHILILATTRSGSSFVGQLFNQHLDVFYLFEPLYHVQNTLIP
                 /db_xref="SPTREMBL:045645"
//db_xref="SPTREMBL:045645"
//translation="MKRQLKLFFIVLITAVVASALTLFITGNSSILGQKSASTGDSKF
DKLNKAYEQIKSDYYQKTDDDKLVDGAIKGMIQSLDDPYSTYMDQEQAKSFDETISAS
FEGIGAQVEEKDGEILLIVSPIKGSPAEKAGIKPRDQIIKVNGKSVKGNNVNEAVALIR
                                                                                                    GKKGTKVKLELNRAGVGNIDLSIKRDTIPVETVYSEMKDNNIGEIQITSFSETTAKEL
TDAIDSLEKKGAKGYILDLRONPGGLMEQAITMSNLFIDKGKNIMQVEYKNGSKEVMK
AEKERKYTKPTVALVNOGTASRSRNYGRCLHESSNVPLIGETFGKGTVQTAKEVDG
STVKLTVAKHLTADGEWIHKKGIKPQVKAELPDYAKLPYLDADKTYKGGTGTNVVA
QKMLKALGYKVKVNSMYDQDFVSVVKQPQKKEKLNETGILTGDTTTKLMIELQKKLSD
NDTQMEKALETLKKEM"
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Human chondroitin 6-sulfotransferase: cloning, gene structure, and
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Bukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalla; Eutheria; Primates; Catarrhini; Hominidae; Homo.
1 (bases 1 to 2190)
Williams, K. J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            HSU65637 2190 bp mRNA PRI 06-AUG-1998
Homo sapiens chondroitin-6-sulfotransferase mRNA, complete cds.
U65637
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/protein_id="AAC28776.1"
/db_xref="G1:2769702"
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Biochim. Biophys. Acta 1407 (1), 92-97 (1998)
98306085
                                                                                                                                                                                                                                                                                                                                                         44.00 Length: . 15
3.143 Gaps: 0
93.333 Percent Identity: 53.333
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/db_xref="taxon:9606"
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US-09-485-529-104 x BSORFRM1
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CSRPVCDPPGPADLVLEEGCVRKCGLLNLTVARABACRERSHVAIKTVRVPEVNDLRA
LVEDPRLALKVIQLVRDPRGILASRSETFRDTYRLMRLWYGTGRRYNLDVDLTTV
EDFSNSVSTGLMRPPRIKGKYMLVRYEDLARRPWKKYFEIYGFLGIPLDSHVARLTV
NTRGDPTLGKHKYGTVRNSAATAEKWRFRLSYDIVAFAQNACQQVLAQLGYKIAASEE
ELKNPSVSLVEERDFRPFS"
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RLCEESPTFAYNLSRKTHILILATTRSGSSFVGQLFNOHLDVFYLFEPLYHVONTLIP
RFTQGKSPADRRVMLGASRDLLRSLYDCDLYFLENYIKPPPVNHTTDRIFRRGASRVL
                     LVEDPRLNLKVIQLVRDPRGILASRSETFRDTYRLWRLWYGTGRKPYNLDVTQLTTVC
EDFSNSVSTGLMRPPWLKGKYMLVRYEDLARNPWKKTEEIYGFLGIPLDSHVARWIQN
NTRGDPTLGKHKYGTVRNSAATAEKWRFRLSYDIVAFAQNACQQVLAQLGYKIAASEE
CSRPVCDPPGPADLVLEEGDCVRKCGLLNLTVAAEACRERSHVAIKTVRVPEVNDLRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Submitted (13-MAY-1997) to the DDBJ/EMBL/GenBank databases. Osami Habuchi, Aichi University of Education, Department of Life Science; Igaye-cho, Kariya, Aichi 448, Japan (Tel:0556-36-3111, Fax:0556-36-437)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Molecular cloning and characterization of human keratan sulfate Gal-6-sulfotransferase J. Biol. Chem. 272 (51), 32321-32328 (1997) 98070405
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AB003791 2415 bp mRNA PRI 14-FEB-1998
Homo sapiens mRNA for keratan sulfate Gal-6-sulfotransferase,
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/protein_id="BAA24840.1"
/db_xref="GI:2887403"
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Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
I (Dases I to 2415)
Habuchi, O.
Direct Submission
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Fukuta,M., Inazawa,J., Torii,T., Tsuzuki,K., Shimada,E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 14
Gaps: 0
Percent Identity: 57.143
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keratan sulfate Gal-6-sulfotransferase
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Homo sapiens
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/organism="Homo sapiens"
/db_xref="taxon:9606"
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/dev_stage="fetus"
/map="l1p11.1-11.2"
/tissue_type="brain"
367. .1602
/function="enzyme"
                                                                                                        ELKNPSVSLVEERDFRPFS"
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85.714
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US-09-485-529-104 x HSU65637
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LOCUS AB003791
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LDSRPDCKPOCDTEHGCEDAALKDLSKYEVDLSTGGFULGVLTATKRKYLFAHVGKCPPVH
RPSTYPAKNSMAGINORRPPYRJGSVPEIDVLCAQAVRENMOTVTPCTLKKOYCGKK
KTRTILGTNNFIALAHRAVLSGVTQGFMKKAFNSPIALGKNKFKELQTPVLGRCLEAD
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CPGKNSFLDEAAYCNHLDVLRLLSKTTLTCLGDFKQLHPVGFDSHCYVFDIMPQTQLK
TIWRFGQNICDAIQPDYRDKLMSMVNTTRVTHVEKPVRYGQVLTPYHRDREDDAITID
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ELKDavehnQHpvarpidggvvllrsavpslidvlisgadaspkllahhgpgntgidg
TLWDFESEATKEEVALSAQIIQACDIRRGDAPEIGLPYKLYPVRGNPERVKGVLQNTR
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DPITSVSNTIYSLVIYAQHMVLSYFKSGHPHGLLFLQDQLKFEDMLKVQPLIVYSDDL
VLYAESPTMPNYHWWVEHLNLMLGFQTDPKKTAITDSPSFLGCRIINGRQLVPNRDRI
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LVSVRRGIRGNEVELPDGDYASTALLPTCKEINWVAVASNVLRSRFIIGPPGAGKTYW
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Porcine reproductive and respiratory syndrome virus. Porcine reproductive and respiratory syndrome virus viruses; sRNA positive-strand viruses, no DNA stage; Nidovirales; Arteriviridae; Arterivirus.

1 (bases 1 to 4374)

2 (bases 1 to 4374)

Cloning and expression of PRRSV ORFID and demonstration and characterization of its NTPase activity
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Butlista, B.M. and McGruder, E.D.
Direct Submission
Submitted (23-AUG-2000) Biology Research and Development, Elanco
Animal Health, a Division of Eli Lilly and Company, 2001 West Main
St, Greenfield, IN 46140, USA
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AF298771 4374 bp RNA VRL 09-OCT-2000 Porcine reproductive and respiratory syndrome virus RNA-dependent

    .4374
/organism-"Porcine reproductive and respiratory syndrome

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/note="ORF1b; zinc-finger protein; helicase (NTPase);
expression of ORF1b occurs due to an upstream ribosomal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /product="RNA-dependent RNA polymerase"
/protein_id="AAG22078.1"
/db_xref="G1:10719656"
                                                                                                                                                                                                                                                                                                                                                                                                    1498 CAGGTGCTGGCCTGGGCTACAAGATCGCCGCCTCGGAG 1539
                                                                                                                                                               Gaps: 0
Percent Identity: 57.143
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  486
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  687
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US-09-485-529-104 x AB003791
  805
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LOCUS AF298771
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                                                                                                                                                            Ratio:
Percent Similarity:
                                                                                                                                    Quality:
  437
                                                                                                           alignment_scores:
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AASLPHAFIGDVKGTTVGGCHHVTSRYLPRVLPKESVAVVGVSSPGKAAKALCTLTDV
YLPDLEAYLLPETQSKCWKMILDFKBVRLAVWKDKTAXFQLEGRYFTWYQLASYSYI
YRPVNSTYYLLDPCMGPALCNRVVGSTHWGADLAVTPYDYGKIILSSAYHGEMPPGY
KILACAEFSLDDPVKYKHTWGFESDTAYLYEFTGNGEDWEDYNDAFRARQEGKIYKAT
ATSLKFYFPPGPVIEPTLGLN"
NLAVHRDGQLIVLDRNNKECTVAQALGNGDKFRATDKRVVDSLRAICADLEGSSSPLP
KVAHNLGFYFSPDLTQFAKLPVELAPHWPVVTTQNNEKWPDRLVASLRPIHKYSRACI
                                          GAGYMVGPSVFLGTPGVVSYYLTKFVKGEAQLLPETVFSTGRIEVDCREYLDDREREV
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CEEV spheroidin.
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Arabidopsis S
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Arabidopsis
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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    protein search, using sw model

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                                                                                                                The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by glibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with glibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being glibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit glibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a glibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents
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This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be
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Claim 1; Page 53; 88pp; English.
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expressed
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ID AAY02

AC AAY02

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XX BH G
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used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the wheat Rht clone 5al genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the partial sequence of the maize D8-1 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     The specification describes polypeptides encoded by the Rht gene (and
                                                                                                                                                                                                                                                                                                           Gaps
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is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Protein encoded by the partial sequence of the maize D8-1 allele.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                              Length 623;
                                                                                                                                                                                                                                                                                                      0; Indels
                                                                                                                                                                                                                                                            100.0%; Score 81; DB 20;
100.0%; Pred. No. 1e-06;
ive 0; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      AAY02542 standard; Protein; 100 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Fig 11b; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      97GB-0017192.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              98WO-GB02383
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                     Query Match 100.
Best Local Similarity 100.
Matches 17; Conservative
                                                                                                                                                                                                                                                                                                                                                 1 DELLAALGYKVRASDMA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          paclobutrazol; maize
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI: 1999-181040/15
                                                                                                                                                                                                623 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           N-PSDB; AAX36281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         16-JUL-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           W09909174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      13-AUG-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAY02542;
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                                                                                                                                                                                                    Sequence
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                                                                                                                                                                                                                                                                                                                                                                                           38
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST.

Protein encoded by rice EST D39460 sequence.

(first entry)

16-JUL-1999

AAY02538;

AAY02538 standard; Protein; 256 AA.

AAY02538

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22 dellaalqykvrssdma 38

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence is encoded by the partial sequence of the maize D8-2023 allele.
                                                                              Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                         Protein encoded by the partial sequence of the maize D8-2023 allele.
                                                                                                                                                                                                                                                                                                                                                        Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                              ;
0
                                             Length 100;
                            Score 78; DB 20; Length Lu. Pred. No. 4.7e-07;
                                                                            1; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig 11d; 88pp; English.
                                                                                                                                                                                                                         AAY02543 standard; Protein; 123 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Richards
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (PLAN-) PLANT BIOSCIENCE LTD.
                                            96.3%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           98WO-GB02383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         97GB-0017192
                                                                                                                                                                                                                                                                                         16-JUL-1999 (first entry)
                                                                                                          1 DELLAALGYKVRASDMA 17
                                                                                                                               34 dellaalgykvrssdma 50
                                                                            16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                        paclóbutrazol; maize.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WPI; 1999-181040/15.
N-PSDB; AAX36282.
                                            Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Sequence 123 AA;
100 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         07-AUG-1998;
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                                                                                                                                                                                                                                                       AAY 02543;
Sequence
                                                                                                                                                                                                                                                                                                                                                                                                                            Zea mays
                                                                            Matches
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which

New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype

Claim 12; Fig 6b; 88pp; English.

Richards DE;

Peng J,

Harberd NP,

WPI; 1999-181040/15.

N-PSDB; AAX36277

(PLAN-) PLANT BIOSCIENCE LTD.

97GB-0017192.

13-AUG-1997; 07-AUG-1998;

WO9909174-A1.

25-FEB-1999

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Assitivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of gibberellin biosynthesis; such as paclobutrazol, c.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by crice expressed sequence tag (EST) AAD39460, which is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length 256;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 78; DB 20; Lv
Pred. No. 1.4e-06;
1; Mismatches 0;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAY02541 standard; Protein; 630 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DELLAALGYKVRASDMA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match 96.3
Best Local Similarity 94.1
Matches 16; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      256 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence
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ID AAY0
XX
AC AAY0
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Gaps

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Score 78; DB 20; Length 123; Pred. No. 6e-07; 1; Mismatches 0; Indels

96.38;

1 Similarity 94.1%;
16; Conservative

Query Match Best Local Similarity

Matches

DELLAALGYKVRASDMA 17

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W09909174-A1

Zea mays.

25-FEB-1999

07-AUG-1998;

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990S-0134256.
990S-0134218.
990S-0134219.
990S-0134221.
990S-0134370.
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99US-0132048.
99US-0132407.
99US-0132484.
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99US-0132486.
99US-0132487.
99US-0132863.
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990S-0135124.
990S-0135353.
990S-0135629.
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99US-0136392.
99US-0136782.
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99US-0138540.
99US-0138847.
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99US-0139452.
99US-0139453.
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99US-0139455.
99US-0139456.
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99US-0139458.
99US-0139459.
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99US-0137528.
99US-0137502.
99US-0137724.
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                                                                                  2000EP-0301439
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99US-0128714
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99US-0139817
Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                     30-APR-1999;
04-MAY-1999;
05-MAY-1999;
06-MAY-1999;
06-MAY-1999;
07-MAY-1999;
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16-JUN-1999;
16-JUN-1999;
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18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
18-JUN-1999;
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30-APR-1999;
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14 -MAY -1999;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence is encoded by the maize lal genomic clone sequence.
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                                                             Rht gene; homologue; Triticum aestivum; wheat; growth inhibition;
antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
paclobutrazol; maize.
                                                                                                                                                                                                                                                                                                                                                                New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                       Protein encoded by maize lal genomic clone sequence.
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N-PSDB; AAX36280.
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Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter; termination sequence.

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28-JUN-1999; 99US-01 29-JUN-1999; 99US-01 30-JUL-1999; 99US-01 01-JUL-1999; 99US-01 02-JUL-1999; 99US-01 06-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	28 JUN-1999; 99US-01 29-JUN-1999; 99US-01 30-JUN-1999; 99US-01 01-JUL-1999; 99US-01 02-JUL-1999; 99US-01 08-JUL-1999; 99US-01 08-JUL-1999; 99US-01	24 - JUN	σ	9US-01				
29.JUN-1999; 99US-01 30.JUN-1999; 99US-01 01.JUL-1999; 99US-01 02.JUL-1999; 99US-01 06.JUL-1999; 99US-01 09.JUL-1999; 99US-01	29-JUN-1999; 99US-01 30-JUN-1999; 99US-01 01-JUL-1999; 99US-01 02-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	28-JUN	σ	9US-01				
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01-00L-1999; 990S-01 02-JUL-1999; 99US-01 06-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	01-00L-1999; 990S-0] 01-00L-1999; 990S-0] 06-00L-1999; 990S-0] 08-00L-1999; 990S-0]	30-JUN	σ,	9us-01				
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02-JUL-1999; 99US-01 06-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	02-JUL-1999; 99US-01 06-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	01-JUL	σ,	9us-01				
06-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	06-JUL-1999; 99US-01 08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	02-JUL	σ	90S-01				
08-JUL-1999; 99US-01	08-JUL-1999; 99US-01 09-JUL-1999; 99US-01	06-JUL	9	9us-01				
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990S - 0142977 - 9990S - 0142977 - 9990S - 0143642 - 9900S - 014400S - 9900S - 0144085 - 9900S - 0144085 - 9900S - 0144331 - 9900S - 0144331 - 9900S - 0144332 - 9900S - 0145919 - 9900S - 0149929 - 9900S - 0153363 - 9900S - 0153468 - 9900S - 0153486 - 9900S - 0155486 - 9900S - 01554

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The present sequence is given in a specification relating to the structure and function of a regulatory gene, SCARECROW (SCR).

SCARECROW-like (SCL) genes encoding protelus containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing transgenic plants whose cell division is modified and root and/or stem development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistance in root or embryos and genes encoding starch, lignin or cellulose biosynthesis in shoots. The SCR gene also confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers for a quantitative trait e.g. root or gravitropism trait in molecular
                                             Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Arabidopsis thaliana gibberellin insensitivty gai gene product.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       86.4%; Score 70; DB 21; Length 531;
82.4%; Pred. No. 9.7e-05;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gibberellin insensitivity; gai; plant growth inhibition; dwarf phenotype; lodging resistance; increased yield; flowering regulation; bolting inhibition; spinach; lettuce; antibody; identification; probe; primer; antisense; sense; expression regulation; co-suppression; rice; Bakane disease resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Nucleic acid encoding gibberellin inhibitor GAI and related
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                                                                                                                Claim 14; Fig 13; 200pp; English.
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Best Local Similarity 82.4
Matches 14; Conservative
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N-PSDB; AAT91937.
               WPI; 2000-594315/56.
                                                                                                                                                                                                                                                                                                                                                                                                                                         531 AA;
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Pred. No. 9.5e-05;
2; Mismatches 1; Indels
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Helariutta Y, Bruce W, Lim J;
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99US-0160767.
99US-0160768.
                                                                         99US-0158232.
99US-0158369.
99US-0159293.
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99US-0161404.
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                             99US-0157753
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99US-0162142
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Best Local Similarity
Matches 14; Conserv
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                                                                         08-0CT-1999;
12-0CT-1999;
13-0CT-1999;
13-0CT-1999;
13-0CT-1999;
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14-0CT-1999;
14-0CT-1999;
18-0CT-1999;
21-0CT-1999;
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22-OCT-1999;
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28-OCT-1999
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AAB28575
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õ g (RIEC/) RIECHMANN J L.

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                                                                          The present sequence is the Arabidopsis thaliana gibberellin insensitivity (gai) gene product (GAI), the expression of which inhibits plant growth. However the inhibition is antagonised by gibberellin (GA), while gai expression confers a dwarf phenotype gibberellin (GA), while gai expression confers a dwarf phenotype confers that is insensitive to GA. Manipulating gai and GAI expression can produce tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit bolting in spinach and lettuce. GAI can be used to raise specific antibodies for itequences, or also be used as process or primers to identify and clone related sequences, or in the preparation of antisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI may be resistant to Bakane disease. Manipulation of gai and GAI makes it possible to tallor the degree of dwarfism and GAI makes it possible to tallor the degree of dwarfism
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antisense sequences - used to create tall, or particularly, dwarf plants, especially crops such as maize, rice and wheat
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                                                                                                                                                                                                                                                                                                                                                                                                                        ; DB 18; Length 532; . 9.7e-05;
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Pred. No. 9.7e-
2; Mismatches
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270..274
/note= "Conserved domain"

    A. thaliana transcription factor G308.

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                                               Claim 1; Fig 4; 76pp; English
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22-AUG-2000; 2000US-0227439.
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Best Local Similarity 82.4
Matches 14; Conservative
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PILGRIM M.
ADAM L.
                                                                                                                                                                                                                                                                                                                                                                           532 AA;
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HEARD J.
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The patent relates to polynucleotides encoding 35 plant transcription factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the control and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, response, wounding response, cell cycle regulation, pigmentation, flowering and senescence of plants and for modifying sink-source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and physical and seed to alter the structure and developmental
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onlon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. The present sequence is an Arabidopsis thallana transcription factor.
                                                                                                                                                                        Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transcription factor; biochemical characteristic; controlling element; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology; plant trait modification.
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                                                                    Riechmann JL;
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                                                                    Pineda O, Pilgrim M, Adam L,
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Pred. No. 9.7e-05;
2; Mismatches 1;
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270..274
/label= Conserved_domain
                                                                                                                                                                                                                                                    Claim 4; Page 74-76; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 AAE01907 standard; Protein; 532 AA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              86.4%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27 dellavlgykvrssema 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ouery Match
Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DELLAALGYKVRASDMA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thallana
                                                                                                                         WPI; 2001-335977/35.
                                                                    Heard J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         532 AA;
                                (SAMA/) SAMAHA R.
                                                                                                                                            N-PSDB; AAD06646
                                                                                       Samaha R;
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                                                                    Jiang C,
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                                                                                       ru G,
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EP1033405-A2.
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30-APR-1999
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  The present sequence is Arabidopsis thaliana transcription factor, G308, a homologue of G307. The transcription factor is used for altering a plant's biochemical characteristics. The transcription factor may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, such as soybean, wheat, corn, totaton, rice, oilseed rape, such as soybean, wheat, corn, totaton, collised rape, strawberry, raspberry, cartaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, pepplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, gatermelon, rosaceous fruits and/or vegetable brassicas. Transcription factors are key controlling elements of biological pathways and altering the plants of 1 or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor levels in plants offers great potential in agricultural
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Protein identification; signal transduction pathway; metabolic pathway; hybridisation assay; genetic mapping; gene expression control; promoter;
                                                                                                                                                                                                                                                       Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     0; Gaps
                                                                                                                                                                                        Samaha R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 70; DB 22; Length 532;
Pred. No. 9.7e-05;
2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Arabidopsis thaliana protein fragment SEQ ID NO: 47610.
                                                                                                                                                                                        Adam L, Riechmann JL, Heard J,
), Jiang C;
                                                                                                                                                                                                                                                                                                   Claim 4; Page 114-115; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AAG38575 standard; Protein; 533 AA.
                                                               MENDEL BIOTECHNOLOGY INC.
                    17-NOV-1999; 99US-0166228.
17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               86.4%;
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14-NOV-2000; 2000WO-US31344
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    is useful in gene therapy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 DELLAALGYKVRASDMA 17
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                ADAM L.
RIECHMANN J L.
                                                                                                                                                                                       Creelman R, Yu G, Ad
Pilgrim M, Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 termination sequence
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                                                                                                                                                                                                                      WPI; 2001-335999/35.
N-PSDB; AAD05791.
                                                                           CREELMAN R.
                                                                                                                     HEARD J.
SAMAHA R.
PILGRIM M.
PINEDA O.
JIANG C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAG38575;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence
                                                                                                                                 (SAMA/)
(PILG/)
(PINE/)
(JIAN/)
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(ADAM/)
(RIEC/)
(HEAR/)
                                                                 MEND-)
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99US-0132486.
99US-0132487.
99US-0132863.
99US-0134256.
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990S-0134768.
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990S-0135124.
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990S-0139119.
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990S-0139492.
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990S-0139459.
990S-0139460.
990S-0139461.
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99US-0130891.
99US-0131449.
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99US-0132484.
99US-0132485.
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99US-0136782.
99US-0137222.
99US-0137528.
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99US-0137724.
99US-0138094.
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99US-0139750.
99US-0139763.
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99US-0139899.
99US-0140353.
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25-FEB-2000; 2000EP-0301439
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RR 01-JUL-1999; 99US-0141842.

RR 02-JUL-1999; 99US-0142154.

RR 02-JUL-1999; 99US-0142154.

RR 12-JUL-1999; 99US-0142297.

RR 13-JUL-1999; 99US-0142297.

RR 13-JUL-1999; 99US-0142297.

RR 15-JUL-1999; 99US-0144297.

RR 15-JUL-1999; 99US-0144297.

RR 15-JUL-1999; 99US-0144297.

RR 19-JUL-1999; 99US-0144484.

RR 19-JUL-1999; 99US-0144484.

RR 19-JUL-1999; 99US-0144484.

RR 19-JUL-1999; 99US-0144213.

RR 19-JUL-1999; 99US-0144213.

RR 19-JUL-1999; 99US-0144213.

RR 19-JUL-1999; 99US-0144213.

RR 22-JUL-1999; 99US-0144213.

RR 22-JUL-1999; 99US-0145218.

RR 22-JUL-1999; 99US-0145218.
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Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL; transgenic plant; cell division; molecular marker; herbicide resistance; salt resistance; pathogen resistance; insect resistance.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                    86.4%; Score 70; DB 21; Length 533;
82.4%; Pred, No. 9.8e-05;
ive 2; Mismatches 1; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAB28574 standard; Protein; 587 AA.
9905 - 0154039
9905 - 0154039
9905 - 0155139
9905 - 0155136
9905 - 0155486
9905 - 0155486
9905 - 0156569
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Arabidopsis SCLa8.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WO200053723-A2
16-SEP-1999

22-SEP-1999

23-SEP-1999

24-SEP-1999

28-SEP-1999

29-SEP-1999

06-OCT-1999

07-OCT-1999

13-OCT-1999

13-OCT-1999

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Local
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Matches
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  9
Pb
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The present sequence is given in a specification relating to the structure and function of a regulatory gene, SCARECROW (SCR).

SCARECROW-like (SCL) genes encoding proteins containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing transgenic plants whose cell division is modified and root and/or stem development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or thinner root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistence in root or embryos and genes encoding starch, lighth or cellulose biosynthesis in shoots. The SCR gene also confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers
                                                                                                                                                                                                                       Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance
                                                                                      Di Laurenzio L, Wysocka-Diller J, Malamy JE, Pysh L;
Y, Bruce W, Lim J;
                                                                                                                                                                                                                                                                                                                Claim 14; Fig 13; 200pp; English.
99US-0265585
                                          (UYNY ) UNIV NEW YORK STATE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       breeding of crop plants
                                                                                                                                                   WPI; 2000-594315/56.
                                                                                                                                                                               N-PSDB; AAC65291
                                                                                                           Helariutta Y,
10-MAR-1999;
                                                                                         Benfey PN,
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587 AA; Seguence

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 Score 70; DB 21; Length 587;
Pred. No. 0.00011;
                              1; Indels
                              2; Mismatches
 86.4%;
82.4%;
Query Match 86.4
Best Local Similarity 82.4
Matches 14; Conservative
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1 DELLAALGYKVRASDMA 17 g δ

AAE02560 standard; Protein; 587 AA. AAE02560; AAE02560 RESULT THE STATE OF STATE OF

(first entry) 10-AUG-2001 A. thaliana transcription factor G308 homolog, G307.

Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germination; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; pigmentation; flowering; senescence; physiology; storage organ; metabolism

Arabidopsis thaliana.

Location/Qualifiers 323..339 /note= "Conserved domain"

Domain

WO200135725-A1

25-MAY-2001.

14-NOV-2000; 2000WO-US31414

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The patent relates to polynucleotides encoding 35 plant transcription factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the cohract proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, response, wounding response, cell cycle regulation, pigmentation, ilowering and senescence of plants and for modifying sink-source relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, colfee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, the characteristics of pares or plants plants in the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, confiee, cucumber, eggplant, grape, carrot, cauliflower, confiee, characteristics of plants plants plants, pass, honey dew, lettuce, mango, melon, confiee, cucumber, eggplant, grape, pass, peppers, princapple, spinach, squash, sweet corn, confiee, cucumber, eggplant, grape, pass, peppers, princapple, spinach, squash, sweet corn, confiee, cucumber, eggplant, grape, carrot, cantalone, corn, confiee, cucumber, eggplant, grape, pass, peppers, carrot, cantalone, corn, confiee, cucumber, pass, peppers, pass, peppers, carrot, cantalone, corn, confiee, cucumber, eggplant, grape, carrot, cantalone, corn, confiee, cucumber, eggplant, grape, carrot, cantalone, corn, control cantalone, cantalone, corn, control cantalone, cantalone, corn, control cantalone, cantalone, corn, cor
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Riechmann JL;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ), Heard J, Pineda O, Pilgrim M, Adam L,
Samaha R;
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Pred. No. 0.00011;
2; Mismatches 1;
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                                                                                                                                                                   MENDEL BIOTECHNOLOGY INC
                                   17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-335977/35.
N-PSDB; AAD06661.
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HEARD J.
PINEDA O.
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Search completed: December 19, 2001, 17:07:10 Job time: 206 sec

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GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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OM protein - protein search, using sw model

; Search time 12.86 Seconds
(without alignments)
100.697 Million cell updates/sec December 19, 2001, 17:05:49 Run on:

US-09-485-529-104 81 1 DELLAALGYKVRASDMA 17 Perfect score: Sequence: Title:

BLOSUM62 Gapop 10.0 , Gapext 0.5 Scoring table:

219241 seqs, 76174552 residues Searched:

Total number of hits satisfying chosen parameters:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100%

Listing first 45 summaries

PIR 68:* Database :

pirl:* pir2:* pir3:* pir4:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result	Š	Query		9	4	10000
2	arose	Marci	rendru			Describtion
1	7.0	86.4		7	696688	hypothetical prote
7	7.0	86.4		~	T51475	
က	20	86.4	533	7	н86282	protein F10B6.34 [
4	7.0	86.4	587	~	D84426	hypothetical prote
'n	46	56.8	495	~	C71679	UDP-n-acetylmurama
9	45	55.6	257	~1	T10758	mandelonitrile lya
7	44	54.3	466	~	B69610	carboxy-terminal p
œ	43	53.1	640	~	E64116	exodeoxyribonuclea
σ	42	51.9	263	7	T01149	probable acetone-c
10	42	51.9	516	7	E96839*	hypothetical prote
11	41	50.6	272	~	C72498	probable stress pr
12	41	50.6	311	N	A75047	erate c
13	41	50.6	314	~	B71114	probable ferredoxi
14	41	50.6	454	ď	B70418	UDP-N-acetylmurama
15	41	50.6	463	7	D81960	ATP-dependent DNA
16	41	50.6	469	N	B81201	UDP-N-acetylmurama
17	41	50.6	484	N	C84955	UDP-N-acetylmurama
18	41	50.6	491	, -	CEECAM	UDP-N-acetylmurama
19	41	50.6	491	~	G85491	hypothetical prote
50	41	50.6	206	~	A81777	UDP-N-acetylmurama
21	41	50.6	550	N	T37519	probable amino aci
22	41	٥.	1002	7	S70292	FUN12 protein - ye
23	40	49.4	96	~	683600	hypothetical prote
. 24	40	49.4	330	~	A83417	probable oxidoredu
25	40	49.4	477	7	E82763	UDP-N-acetylmurama
56	40	49.4	480	~	D83094	UDP-N-acetylmurama
27	40	49.4	700	~	T49445	adrenoleukodystrop
28	40	49.4	957	7	T10633	hypothetical prote
59	39	48.1	82	7	A72274	

conserved hypothet	probable (S)-aceto	probable ribosomal	hypothetical prote	hypothetical prote	probable acetone-c	2,2',3-trihydroxyb	probable molybdenu	pyruvate synthase	spermidine/putresc	spermidine/putresc	hypothetical prote	spermidine/putresc	probable UDP-N-ace	hypothetical prote	cholecystokinin ty
H75570	T02428	A71186	876919	F83609	T01151	A49932	H81448	T45086	F82201 '	A40840	F85683	B64118	C71338	B84221	T19135
7	α	~	~	7	~	7	~	7	~	7	~	7	7	7	7
136	141	188	194	250	263	294	294	311	377	378	378	381	481	604	643
48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1	48.1
39	33	33	39	33	33	39	33	39	39	39	39	39	39	39	33
30	31	32	33	34	35	36	37	38	39	40	41	42	43	44	45

ALIGNMENTS

696688

C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
C;Date: 02-Mar-2001
C;Date: 02-Mar-2001
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Hudhes, B.; Hudrar, L.
Chin, C.W.; Stoney, C.; Khan, S.; Khaykin, E.; Kim, Rithers: Marchory, T.; Rouney, T.; Rouney, T.; Schwartz, J.R.; Shinn, P.; Southwick, A.W.; Sun, H.; Tallo Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Thle: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
A;Reference number: A86141; MuID:21016719
A;Retaus: preliminary
A;Retaus: preliminary
A;Molecule trace. Dava

A;MOlecule rype: DNA A;Residues: 1-511 <STO> A;Cross-references: GB:AE005173; NID:g10092507; PIDN:AAG12907.1; GSPDB:GN00141 C;Genetics:

A; Gene: T27F4.10 A; Map position: 1

Gaps ö Length 511; Score 70; DB 2; Length 511 Pred. No. 0.00017; 1; Mismatches 2; Indels 86.4%; 82.4%; Ouery Match 86.4 Best Local Similarity 82.4 Matches 14; Conservative

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32 DELLVVLGYKVRSSDMA 48 1 DELLAALGYKVRASDMA 17 ò

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7 RESULT

RGA-like protein - Arabidopsis thaliana
N;Alternate names: protein K3M16_60
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 18-Aug-2000 #sequence_revision 18-Aug-2000 #text_change 18-Aug-2000
C;Accession: T51475
R;Sato, S.; Nakamura, Y.; Kaneko, T.; Kato, T.; Asamizu, E.; Kotani, H.; Tabata, S.; submitted to the Protein Sequence Database, August 2000
A;Reference number: Z25394
A;Reference number: Z53394
A;Status: preliminary

A;Molecule type: DNA *

A;Residues: 1-523 <SAT>
A;Cross-references: EMBL:AL391150
A;Experimental source: cultivar Columbia; BAC clone K3M16

a

86.4%;

Query Match 86.4 Best Local Similarity 82.4 Matches 14; Conservative

C;Genetics: A;Map position: 5 A;Note: K3M16_60

8

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RESULT H86282

1 DELLAALGYKVRASDMA 17

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N;Alternate names: hydroxynitrile lyase
C;Species: Hevea brasiliensis (Para rubber tree)
C;Accession: 10758
C;Accession: 10758
R;Hasslacher, M.; Schall, M.; Hayn, M.; Griengl, H.; Kohlwein, S.D.; Schwab, H.
J. Biol. Chem. 271, 5884-5891, 1996
A;Title: Molecular-cloning of the full-length cdna of (s)-hydroxynitrile lyase from h
                                                                                                                                                                                                                                                                                                               UDP-n-acetylmuramate--alanine ligase (murc) RP247 - Rickettsia prowazekii C; Species: Rickettsia prowazekii C; Species: Rickettsia prowazekii C; Species: Rickettsia prowazekii C; Date: 21-Nov-1998 #sequence_revision 21-Nov-1998 #text_change 03-Nov-2000 C; Accession: C71679 Rs. Andersson, S.G.E.; Zomorodipour, A.; Andersson, J.O.; Sicheritz-Ponten, T.; Alsmark Nature 396, 133-140, 1998 Aritita prowazekii and the origin of mitochondria. A; Reference number: A71630; MUID:99039499 A; Reference number: A71679 A; Recession: C71679 A; Recession: C71679 A; Stelliminary; nucleic acid sequence not shown; translation not shown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A; Description: catalyzes the conversion of mandelonitrile to benzaldehyde and cyanide A; Note: involved in the biodegradation of cyanogenic glycosides; also catalyzes the s C; Keywords: aldehyde-lyase; carbon-carbon lyase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       A;Molecule type: DNA
A;Residues: 1-495 <AND>
A;Cross-references: GB:AJ335271; GB:AJ235269; NID:g3868717; PIDN:CAA14709.1; PID:g386
A;Experimental source: strain Madrid E
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A;Molecule type: mRNA
A;Residucs: 1-257 <HAS>
A;Cross_references: EMBL:U40402; NID:g1223883; PIDN:AAC49184.1; PID:g1223884
                                 Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Score 46; DB 2; Length 495;
Pred. No. 3.1;
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                                 Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          mandelonitrile lyase (EC 4.1.2.10) – Para rubber tree
Pred. No. 0.00019;
2; Mismatches 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     C; Superfamily: UDP-N-acetylmuramate--alanine ligase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Mismatches
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A; Accession: T10758
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   56.8%;
60.0%;
   82.48;
                                                                                                                                  44 DELLAVLGYKVRSSEMA 60
                                                                                                1 DELLAALGYKVRASDMA 17
                                 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Similarity 66.7
10; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      |:| |||||: ||:
31 EILHNLGYKVQGSDL 45
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELLAALGYKVRASDM 16
Best Local Similarity
Matches 14; Conserva
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     n active-site residue.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         C;Genetics:
A;Gene: murC; RP247
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Matches
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  C;Accession: H86282
R;Theologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alonso, Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; ansen, N.F.; Hughes, B.; Huizar, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, K.; Nature 408, 816-820, 2000
A;Authors: Hungher, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C. C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marziali, Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallon, ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Whoney, T.; Rowley, C.; Davis, R.W.
A;Title: Sequence and analysis of Chromosome I of the plant Arabidopsis.
A;Reference number: A86141; MUID:21016719
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    profein F10B6.34 (imported) - Arabidopsis thaliana
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
                                                                                                                                                                                                                                   Gaps
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                                                                                                                                                                Length 523;
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                                                                                                                                                            Score 70; DB 2; Length 523
Pred. No. 0.00017;
1; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1; Indels
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Pred. No. 0.00018;
2; Mismatches 1;
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86.4%;

Query Match
Best Local Similarity 82.4
Matches 14; Conservative

A; Map position: 1

C; Genetics:

Molecule type: DNA Residues: 1-533 <STO>

Status: preliminary

28 DELLAVLGYKVRSSEMA 44

g

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1 DELLAALGYKVRASDMA 17

Length 587;

86.4%; Score 70; DB 2;

Status: preliminary Molecule type: DNA Residues: 1-587 <STO>

A,Gene: At2g01570 A,Map position: 2

C; Genetics:

Query Match

C; Superfamily: exodeoxyribonuclease V 67K chain

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60.0%;
                                    53.1%;
69.2%;
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Best Local Similarity 60.0
Matches 9; Conservative
                                                                                                             Conservative
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LLEALGHRVTALDLA 43
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                                                                                                                                                                                                                                                355 LLATTGYKVEGSD 367
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                                                                                                                                                                               3 LLAALGYKVRASD 15
                                Query Match
Best Local Similarity
Matches 9; Conserv
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A Molecule type: DNA
A Residues: 1-263 <STO>
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                                                      C;Species: Bacillus subtilis
C;Decies: Dispecies: Dispecies
C;Decies: Dispecies: Dispecies
C;Decies: Dispecies: Dispecies
C;Decies: Dispecies: Dispecies
C;Bron, S; Broulllet, S; Bruschi, C.V.; Caldwell, B; Capuano, V.; Carter, N.M.; Chc
A; Ehrlich, S.D.; Emmerson, P.T.; Entlan, K.D.; Errington, J; Fubret, C.; Ferrari, E.
Nature 390, 249-256, 1997
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Foulger, D.; Fritz, C.; Fujita, M.; Fujita, Y.; Fuma, S.; Galizzi, A.; Galler
A;Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Devine, A.; Liu, H.; Masuda, S.; Muncel
Y, M.; Ogawa, K.; Ogiwara, A.; Oudega, B.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
R, Authors: Lauber, J.; Lazarevic, V.; Lee, S.M.; Park, S.H.; Parro, V.; Pohl, T.M.; Portetelle
R, Authors: Lauber, J.; Lazarevic, W.; Tanaka, E.; Roche, B.; Rose, M.; Sekiguchi, J.; Sakowska, A.; Scanlon,
A;Authors: Schleich, S.; Schroeter, R.; Scoffone, F.; Sekiguchi, J.; Sekowska, A.; Sero,
A;Authors: Yoshikawa, H.F.; Zumsteln, E.; Yoshikawa, H.; Danchin, A.
A;Title: The complete genome sequence of the Gram-positive bacterium Bacillus subtilis.
A;Reference number: A69580; MUID:98044033
A;Accession: B69610
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A; Cross-references: EMBL:X98341; NID:g1402943; PIDN:CAA66987.1; PID:g1402944
A; Experimental source: strain PY17
C; Comment: This protein is presumed to be involved in cleavage of the carboxyl-terminal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           A; Cross-references: GB: 299114; GB: AL009126; NID: g2634230; PIDN: CAB13850.1; PID: g2634351 A; Experimental source: strain 168 R; Marasco, R.; Varcamonti, M.; Ricca, E.; Sacco, M. Gene 183, 149-152, 1996 A; Title: A new Bacillus subtilis gene with homology to Escherichia coli prc. A; Reference number: JC5744; MUID: 97149292
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    R;Fleischmann, R.D.; Adams, M.D.; White, O.; Clayton, R.A.; Kirkness, E.F.; Kerlavage, J. Gocayne, J.D.; Scott, J.; Shirley, R.; Liu, L.I.; Glodek, A.; Kelley, J.M.; Weidman, D.M.; Brandon, R.C.; Fine, L.D.; Fritchman, J.L.; Fuhrmann, J.L.; Geoghagen, N.S.M. Science 269, 496-512, 1995
A;Authors: Gnehm, C.L.; McDonald, L.A.; Small, K.V.; Fraser, C.M.; Smith, H.O.; Venter, A;Title: Whole-genome random sequencing and assembly of Haemophilus influenzae Rd.
A;Reference number: A64000; MUID:95350630
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      A;Status: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Residues: 1-640 <TIGR>
A;Cross-references: GB:U32811; GB:L42023; NID:g1574774; PIDN:AAC22967.1; PID:g1574782;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    exodeoxyribonuclease V 67K chain homolog - Haemophilus influenzae (strain Rd KW20)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ö
carboxy-terminal processing proteinase ctpA (EC 3.4.99.-) - Bacillus subtilis
N;Alternate names: tail-specific endopeptidase Prc
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C;Date: 18-Aug-1995 #sequence_revision 18-Aug-1995 #text_change 08-Oct-1999
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Pred. No. 6.6;
4; Mismatches 3; Indels
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Best Local Similarity 53.3
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 A; Molecule type: DNA
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A;Start codon: TTG
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Ritheologis, A.; Ecker, J.R.; Palm, C.J.; Federspiel, N.A.; Kaul, S.; White, O.; Alon Chin, C.W.; Chung, M.K.; Conn, L.; Conway, A.B.; Conway, A.R.; Creasy, T.H.; Dewar, ansen, N.F.; Hughes, B.; Huizar, L.
Nature 408, 816-820, 200
A;Authors: Hunter, J.L.; Jenkins, J.; Johnson-Hopson, C.; Khan, S.; Khaykin, E.; Kim, C.A.; Li, J.H.; Li, Y.; Lin, X.; Liu, S.X.; Liu, Z.A.; Luros, J.S.; Maiti, R.; Marzia Rizzo, M.; Rooney, T.; Rowley, D.; Sakano, H.
A;Authors: Salzberg, S.L.; Schwartz, J.R.; Shinn, P.; Southwick, A.M.; Sun, H.; Tallo Ker, M.; Wu, D.; Yu, G.; Fraser, C.M.; Venter, J.C.; Davis, R.W.
A;Hille: Sequence and analysis of chromosome 1 of the plant Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                  N.Alternate names: hypothetical protein F2686.25
C;Species: Arabidopsis thaliana (mouse-ear cress)
C;Date: 12-Feb-1999 #sequence_revision 12-Feb-1999 #text_change 16-Feb-2001
C;Accession: T01149; G84626
R;Rounsley, S.D.; Kaul, S.; Lin, X.; Ketchum, K.A.; Crosby, M.L.; Brandon, R.C.; Syke submitted to the EMBL Data Library, June 1998
A;Description: Arabidopsis thaliana chromosome II BAC F2686 genomic sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     A;Residues: 1-263 <ROU>
A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242721
A;Cross-references: EMBL:AC003040; NID:g3242700; PID:g3242721
A;Experimental source: cultivar Columbia
R;Lin, X.; Kaul S.; Rounsley, S.D.; Shea, T.P.; Benito, M.I.; Town, C.D.; Fujli, C.Y
M.; Koo, H.; Moffat, K.S.; Cronin, L.A.; Shen, M.; VanAken, S.E.; Umayam, L.; Tallon,
euss, D.; Nierman, W.C.; White, O.; Eisen, J.A.; Salzberg, S.L.; Fraser, C.M.; Venter
Nature 402, 761-768, 1999
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A;Accession: G84626
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C.Date: 02-Mar-2001 #sequence_revision 02-Mar-2001 #text_change 31-Mar-2001
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                                                                           Indels
   Length
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ore 43; DB;
ed. No. 14;
Mismatches
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3; Mismatches
   Score 43;
Pred. No.
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probable ferredoxin oxidoreductase beta subunit - Pyrococcus horikoshii
C;Species: Dial-1998 #sequence_revision 14-Aug-1998 #text_change 20-Jun-2000
C;Accession: B71114
B;Kawarabayasi, Y:; Sawada, M.; Horikawa, Y.; Hino, Y.; Yamamoto, S.; Se
M.; Ohfuku, Y.; Funahashi, T.; Tanaka, T.; Kudoh, Y.; Yamazaki, J.; Kushida, N.; Ogu
DN, Res. 5, 55-76, 1998
A;Title: Complete sequence and gene organization of the genome of a hyper-thermophili
A;Reference number: A71000; MUID:98344137
A;Reference number: A71000; MUID:98344137
A;Status: preliminary: nucleic acid sequence not shown; translation not shown
A;Molecule type: DNA
A;Status: DNA
A;Ressidues: 1-314 «KAMP
A;Ressidues: 1-314 «KAMP
A;Cross-references: GB:AP000003; NID:93236130; PIDN:BAA29772.1; PID:93257089
A;Experimental source: strain O73
A;Cross-references: GB:AP000003
A;Experimental source: strain O73
A;Genetics:
A;Genetics:
A;Genetics:
A;Genetics:
A;Gene: PH0681
C;Superfamily: pyruvate synthase beta chain
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C;Date: 08-May-1998 #sequence_revision 08-May-1998 #text_change 16-Jul-1999
C;Accession: B70418
R;Deckert, G.; Warren, P.V.; Gaasterland, T.; Young, W.G.; Lenox, A.L.; Graham, D.E.;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 392, 353-358, 1998
Afittle: The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.
A;Reference number: A70300; MUID:98196666
A;Accession: B70418
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A;Molecule type: DNA
A;Residues: 1-454 <AQF>
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UDP-N-acetylmuramate--alanine ligase (EC 6.3.2.8) - Aquifex aeolicus
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Pred. No. 15;
1; Mismatches
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Pred. No. 22;
5; Mismatches
66.7%; Pred. No. 15; ive 1; Mismatches
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66.7%;
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  Best Local Similarity 66.7
Matches 8; Conservative
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Best Local Similarity 43.8
Matches 7; Conservative
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                                                                                                                           90 LKALGYKVKGED 101
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C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
C;Date: 20-Aug-1999 #sequence_revision 20-Aug-1999 #text_change 20-Jun-2000
R;Accession: (72498
R;Accession: C;Aug-1999
A;Accession: C72498
A;Accession: C72498
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R;anonymous, Genoscope
Submitted to the EMBL Data Library, July 1999
A;Bescription: Pyrococcus abyssi genome sequence: insights into archaeal chromosome stru
A;Reference number: A75001
A;Accession: A75047
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A;Moleoule type: DNA
A;Residues: 1-272 <KRM>
A;Cross-references: DDBJ:AP000063; NID:g5105654; PIDN:BAA80971.1; PID:g5105659
                                              A; Molecule type: DNA
A; Residues: 1-516 <STO>
A; Cross-references: GB: AE005173; NID: 96503282; PIDN: AAF14658.1; GSPDB: GN00141
C; Genetics:
A; Gene: F23A5.6
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                                                                                                                                                                                                                                                      Length 516
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                                                                                                                                                                                                                                                                                                      4; Indels
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 41; DB 2
Pred. No. 13;
7; Mismatches
                                                                                                                                                                                                                                                 DB 17;
                                                                                                                                                                                                                                                                                                      4; Mismatches
                                                                                                                                                                                                                                                   Score 42;
Pred. No.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Superfamily: pyruvate synthase beta chain Keywords: oxidoreductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Experimental source: strain Orsay
                                                                                                                                                                                                                                                 51.9%;
50.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       :Gene: APE1961
:Superfamily: aldehyde reductase
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        A; Experimental source: strain Kl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Conservative
                                                                                                                                                                                                                                                                                                    Conservative
                                                                                                                                                                                                                                                                                                                                                     1 DELLAALGYKVRASDM 16
                                                                                                                                                                                                                                                                                                                                                                                                   17 DEMLAALNVRAKASSL 32
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 DELLAALGYKVRASDM 16
                                                                                                                                                                                                                                                   Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Query Match
Best Local Similarity
Matches 6; Conserv
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Molecule type: DNA
Residues: 1-311 <KAW>
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Status: preliminary
                         Status: preliminary
  A; Accession: E96839
                                                                                                                                                                              A; Map position: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gene: PAB1473
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
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Genetics

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C: Detectors: Naisseria meningitidis
(C: Species: Naisseria meningitidis
(C: Species: Naisseria meningitidis
(C: Species: Naisseria meningitidis
(C: Date: 05-May-2000 #sequence_revision 05-May-2000 #text_change 02-Feb-2001
(C: Accession: D81960
(C: Accession: D81960
(C: Archiman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morellingin, Mature 404, 502-506, 2000
(C: Archiman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morellingin, Mature 404, 502-506, 2000
(C: Archiman, M.; James, K.D.; Bentley, S.D.; Churcher, C.; Klee, S.R.; Morellingin, Mature 404, 502-506, 2000
(C: Archiman 402, 502-506, 2000
(C: Ar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ö
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Pred. No. 22;
4; Mismatches 2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Query Match 50.6%;
Best Local Similarity 57.1%;
Matches 8; Conservative
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Search completed: December 19, 2001, 17:07:48 Job time: 119 sec

2 ELLAALGYKVRASD 15 |::|:||||:| | 131 EIGSAVGYKVRFTD 144

qq

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				,

us-09-485-529-104.rsp

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December 19, 2001, 17:07:34; Search time 10.2 Seconds (without alignments) 61.108 Million cell updates/sec
GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                    OM protein - protein search, using sw model
                                                                                                                                                                                                                                                      BLOSUM62
Gapop 10.0 , Gapext 0.5
                                                                                                                                                                            US-09-485-529-104
81
1 DELLAALGYKVRASDMA 17
                                                                                                                                                                              Title:
Perfect score:
Sequence:
                                                                                                                                                                                                                                                    Scoring table:
                                                                                                    Run on:
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100059 Total number of hits satisfying chosen parameters:

100059 seqs, 36664827 residues

Searched:

Minimum DB seq length: 0 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0% Maximum Match 100% Listing first 45 summaries

SwissProt_39:* Database : Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

Result		& Ouerv			SUMMARIES	
, . , .	Score	Match	Length	BB	ID	Description
ч	46		495	-	MURC_RICPR	Q9zds8 ricketts1a
7	45		257	Н	HNL_HEVBR	P52704 hevea brasi
m	43	53.1	640	Н	EX5A_HAEIN	P45158 haemophilus
4	41		311	Н	VORB_PYRAB	Q9uyz2 pyrococcus
2	41		311	Н	VORB_PYRHO	058414 pyrococcus
9	41		454	Н	MURC_AQUAE	067373 aquifex aeo
7	41		484		MURC_BUCAI	P57310 buchnera ap
æ	41		491		MURC_ECOLI	escherich
6	41		550	-	YAO8_SCHPO	Q10087 schizosacch
10	41		1002	7	IF2P_YEAST	
11	39		188	٦	RL5_PYRHO	
12	39		293	Н	DBFB_PSEPA	P47243 pseudomonas
	39		311	П	VORB_PYRFU	Q51802 pyrococcus
14	39		378	П	POTA_ECOLI	P23858 escherichia
15	39		381	П	POTA_HAEIN	P45171 haemophilus
16	39		481	٦	MURC_TREPA	
17	38		273	٦	FOLD_MYCGE	_
18	38		325	-	THIL_ECOLI	
13	38		483		MURC_BUCAP	O51926 buchnera ap
20	38		516	Н	YJJI_ECOLI	escherich
21	38	46.9	617	Н	VG31_BPMD2	064225 mycobacteri
22	38		638	-	SYT2_BACSU	P18256 bacillus su
23	38		665	-	TKT_BUCAI	
24	38		705	7	RNR_AQUAE	67834 aquifex a
25	38		1022	-	SCA4_RICCN	
56	38		1079	7	IF2P_SCHPO	
27	38		1538	-	GLSF_PORPU	
28	38		3829	ч	RPOA_LELV	
53	37		130	~	Y73A_ARCFU	P58014 archaeoglob
30	37	ß	146	Н	YPV9_METTF	P29586 methanobact
31	37	45.7	394	-	SYYC_YEAST	
32	37	45.7	455	-	AROA_AGRSP	Q9r4e4 agrobacteri
33	37	45.7	515	-	UDPE_NPVSL	Q88168 spodoptera

P28595 azospirillu P34913 homo sapien	093625 halobacteri P43329 escherichia P45018 haemophilus	Q00109 ictalurid h P96848 mycobacteri		O14055 schizosacch P45066 haemophilus	P95691 sulfolobus
PYRG_AZOBR HYES_HUMAN	IF2P_HALHA HRPA_ECOLI HRPA_HAEIN	VG35_HSVI1 NAT_MYCTU	HEM3_METJA METC_BORAV	SYYC_SCHPO MURC_HAEIN	IF2P_SULAC
~ ~					7
544 554	583 1300 1304	238	292 395	401 475	534
45.7	45.7 45.7 45.7	44.4	44.4	44.4	44.4
37	37 37 37	36 36	36 36	36 36	36
34 35	36 37 38	39 40	41 42	43 44	45

ALIGNMENTS

RESULT

MURC_RICPR MURC_RICPR TD MURC_RICPR AC 092D58; DT 30-MAY-2000 (Rel. 39, Created) DT 30-MAY-2000 (Rel. 39, Last sequence update) DT 30-MAY-2000 (Rel. 39, Last sequence update)	JUD-N-ZUOL (REI. UDP-N-ACETYLMURAMK ACETYLMURAMOYL-L-F MURC OR RP247. Rickettsia prowaze Bacteria; Proteobe Bickettsiaceas.		Nature 396.13 -1 - FUNCTION: -1 - CATALYTIC -1 - PATHWAY: -1 - SUBCELLUI	Thi Det the use mod ent	EMBL, AJ235271; CAA14709.1; InterPro; IPR000713; Mur_ligase. Pfam; PF01225; Mur_ligase; 1. Peptidoglycan synthesis; Cell wall; Cell div ATP-binding; Complete proteome. NP_BIND 120 126 ATP (POTENTIAL) SEQUENCE 495 AA; 54612 MW; 2E18464088FAD	Query Match 56.8%; Score 46; DB 1; Length 495; Best Local Similarity 60.0%; Pred. No. 1.4; Matches 9; Conservative 3; Mismatches 3; Indels 0; Gaps 0;
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2 ELLAALGYKVRASDM 16 |:| |||||:||: 31 EILHNLGYKVQGSDL 45

Gaps

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Length 257; 3; Indels

1;

Score 45; DB 1 Pred. No. 1.1; 2; Mismatches

55.6%;

Conservative

10;

Similarity

LLAALGYKVRASDMA 17

80 207 235 80 S->A: LOSS OF ACTIVITY. 81 C->S: LOSS OF ACTIVITY. 235 H->A: LOSS OF ACTIVITY. 335 H->A: LOSS OF ACTIVITY.

207 2 235 2 80 81 235 2 257 AA;

SEQUENCE MUTAGEN MUTAGEN

ACT_SITE ACT_SITE MUTAGEN

PDB; 6YAS; 13-OCT-99.
PDB; 1QJ4; 10-OCT-99.
InterPro; 1PR000073; Abhydrolase.
InterPro; IPR000379; Est_11p_thioest_actsite.
Pfam; PF00561; abhydrolase; 1.

Lyase; 3D-structure.

us-09-485-529-104.rsp

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Query Match
Best Local (
                                                                                                                                                                                                                                                           Matches
                                                                                                                                                                                                                                                                                                                     g
01-OCT-1996 (Rel. 34, Created)
01-OCT-1996 (Rel. 34, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
(S)-ACETONE-CYANOHYDRIN LYASE (EC 4.1.2.39) ((S)-HYDROXYNITRILE LYASE)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INJURED TISSUES. DECOMPOSES A VARIETIES OF (R) OR (S) CYNOHYDRINS INTO HCM AND THE CORRESPONDING ALDEHYDES AND KETONES. THE NATURAL SUBSPRATE OF THIS ENZYME IS (S)-ACETONE CYANOHYDRIN. CATALYTIC ACTIVITY: (S)-2-HYDROXYISOBUTYRONITRILE = CYANIDE +
                                                                                                                                                                                 Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids I; Malpighiales; Euphorbiaceae; Hevea.
                                                                                                                                                                                                                                                                                                                               "Molecular cloning of the full-length cDNA of (S)-hydroxynitrile lyase from Hevea brasiliensis. Functional expression in Escherichia coll and Saccharomyces cerevisiae and identification of an active site residue.";
                                                                                                                                                                                                                                                                                                                                                                                                                                X-RAY CRYSTALLOGRAPHY (1.9 ANGSTROMS).
MEDLINE-56434327; PubMed-8805565;
Wagner U.G., Hasslacher M., Griengl H., Schwab H., Kratky C.;
Mechanism of cyanogenesis: the crystal structure of hydroxynitrile
lyase from Hevea brasiliensis.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 X-RAY CRYSTALLOGRAPHY (1.72 ANGSTROMS).

BEDLINE-20014021, PubMed--10548044,
Zuegg J., Gruber K., Gugganig M., Wagner U.G., Kratky C.;
Three-dimensional structures of enzyme-substrate complexes of the hydroxynitrile lyase from Hevea brasiliensis.";
Protein Sci. 8:1990-2000(1999).
InvolvPed In CYANOLVED IN CYANOGENESIS, THE RELEASE OF HCN FROM
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          X-RAY CRYSTALLOGRAPHY (1.1 ANGSTROMS).
MEDLINE-99423043; PubMed-10494652;
Gruber K., Gugganig M., Wagner U.G., Kratky C.;
"Atomic resolution crystal structure of hydroxynitrile lyase from Hevea brasiliensis.";
                                                                                                                                                                                                                                                                                        MEDLINE-96215058; Pubmed-8621461;
Hasslacher M., Schall M., Hayn M., Griengl H., Kohlwein S.D.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        -i- SUBUNTT: HOMODIMER.
-i- PTM: THE N-TERMINUS IS BLOCKED.
-i- SIMILARITY: DISTANT RELATIONSHIP WITH TYPE-B
CARBOXYLESTERASE/LIPASE FAMILY.
                                         257 AA.
                                                                                                                                                                                                                                                             SEQUENCE FROM N.A., AND PARTIAL SEQUENCE.
                                                                                                                                       ((S)-HYDROXYNITRILASE) (OXYNITRILASE).
                                                                                                                                                                      Hevea brasiliensis (Para rubber tree).
                                         PRT;
                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 271:5884-5891(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Biol. Chem. 380:993-1000(1999).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Structure 4:811-822(1996).
                                           STANDARD;
                                                                                                                                                                                                                             NCBI_TaxID=3981;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ACETONE.
                                                                                                                                                                                                                                                                                                                          Schwab H.;
                                         HNL_HEVBR
P52704;
            RESULT 2
HNL_HEVBR
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                                                                                                                                                                                                                                                                                           MEDLINE=95350630; PubMed=7542800; Relation R.A., Kirkness E.F., Fleischmann R.D., Addam M.D., White O., Clayton R.A., Kirkness E.F., Ferischmann R.D., Addam M.D., White O., Clayton R.A., Merrick J.M., McKenney K., Sutton G., Fitzhugh W., Fields C.A., Gocayne J.D., Scott J.D., Shirley R., Liu L.-I., Glodek A., Kellay J.M., Weidman J.F., Phillips C.A., Spriggs T., Hedblom E., Cotton M.D., Utterback T.R., Hanna M.C., Nguyen D.T., Saudek D.M., Brandon R.C., Fitchman J.L., Fuhrmann J.L., Geoghagen N.S.M., Venter J.C.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Haemophilus influenzae.
Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Haemophilus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             "Whole-genome random sequencing and assembly of Haemophilus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SUBUNIT: CONSIST OF THREE SUBUNITS; RECB, RECC AND RECD
                                                                                                                    01-NOV-1995 (Rel. 32, Created)
01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
EXODEOXYRIBONUCLEASE V ALPHA CHAIN (EC 3.1.11.5).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PHOSPHOOLIGONUCLEOTIDES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Science 269:496-512(1995)
                                                                                           STANDARD;
11 |||:|| | 1:|
25 LLEALGHKVTALDLA 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (BY SIMILARITY).
                                                                                                                                                                                                                                                                                    SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                      NCBI_TaxID=727;
                                                                                                                                                                                        RECD OR HI1322
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 influenzae Rd.
                                                                                        EX5A_HAEIN
P45158;
                                                          RESULT 3
EX5A_HAEIN
```

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EMBL; U40402; AAC49184.1; -.

1YAS; 16-JUN-97. 2YAS; 13-OCT-99. 3YAS; 13-OCT-99. 4YAS; 13-OCT-99. 5YAS; 13-OCT-99.

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NCBI_TaxID=63363;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Aquifex aeolicus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          MURC OR AQ_1360.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MURC_AQUAE
067373:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      MURC_AQUAE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ŏ
                                                                                                                                                                                                                                                                                                                                                                                                                                          g
                                                                                                                                                                                                                                                                                                                                                                                                                                                             This SWISS-PROT entry is copyright. It is produced through a collaboration between the Swiss Institute of Bioinformatics and the EMBL outstation the European Bioinformatics Institute. There are no restrictions on its muse by non-profit institutions as long as its content is in no way modified and this statement is not removed. Usage by and for commercial entities requires a license agreement (See http://www.isb-sib.ch/announce/
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                 Hydrolase; Nuclease; Exonuclease; Endonuclease; Helicase; ATP-binding;
DNA repair; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                     Submitted (JUL-1999) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                'Pyrococcus abyssi genome sequence: insights into archaeal chromosome
                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
                                                                                                                                                                                                                                                                                                                            Archaea, Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=29292;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-MAY-2000 (Rel. 39, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORB (EC 1.....) (VOR) (2-OXOISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-
                                                                                                                                                                                                                                                  20-AUG-2001 (Rel. 40, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORB (EC 1.....) (VOR) (2-
OXOLSOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-
FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ö
                                                                                                                       ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       50.6%; Score 41; DB 1; Length 311; 66.7%; Pred. No. 6.8; 1; Mismatches 3; Indels
                                                                                                 53.1%; Score 43; DB 1; Length 640; 69.2%; Pred. No. 6.2;
                                                                                                                       Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Complete proteome.
A3; 34759 MW; 1EBE2609519DAC30 CRC64;
                                                      TP (POTENTIAL).
C3C530AC398B5DA0 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               311 AA.
                                                                                                                                                                                                                       311 AA.
                                                                                                                      0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             or send an email to license@isb-sib.ch).
                                                       ATP
                                                                                                                                                                                                                                                                                                                                                                                                                                          GAMMA CHAIN (BY SIMILARITY).
                                                                                                                                                                                                                                        20-AUG-2001 (Rel. 40, Created)
                                                                640 AA; 72864 MW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    EMBL; AJ248287; CAB50270.1; -
 U32811; AAC22967.1;
P09980; IUAA.
                                                                                                                                                                                                                                                                                                                                                                                                            structure and evolution."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ouery Match
Best Local Similarity 66.7
                                                                                                                       Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               STANDARD;
                                                                                                                                                                                                                       STANDARD;
                                                       201
                                                                                                                                                                355 LLATTGYKVEGSD 367
                                                                                                                                            3 LLAALGYKVRASD 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        90 LKALGYKVKGED 101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    4 LAALGYKVRASD 15
                                                                                     Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          311 AA;
                                                                                                                                                                                                                                                                                                                      Pyrococcus abyssi.
                                                                                                                                                                                                                                                                                                                                                                SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase;
SEQUENCE 311
EMBL; U32811; PHSSP; P09980; 1
                                                                                                                                                                                                                                                                                                           VORB OR PAB1473
                                                                                                                                                                                                                                                                                                                                                                           STRAIN-ORSAY;
                                                                                                                                                                                                                    VORB_PYRAB
Q9UYZ2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              VORB_PYRHO
058414;
                                                                                                                                                                                                                                                                                                                                                                                      Heilig R.;
                                                                SEQUENCE
                                                      NP_BIND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         RESULT 5
VORB_PYRHO
                                                                                                                                                                                                           VORB_PYRAB
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               884444B
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                                                                                                                                                                                                                                                                         MEDLINE-98344137; PubMed-9679194;
Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y.,
Kawarabayasi Y., Sawada M., Horikawa H., Hasoyama A., Nagai Y.,
Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y.,
Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A.,
Aoki K., Tsohizawa T., Nakamura Y., Robb F.T., Horikoshi K.,
Masuchi Y., Shizuya H., Kikuchi H., Shizuya Sarabacterium, Pyrococcus horikoshii OT3.";
DNA Res. 5.55-76[1998].
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                                                                              Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBI_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  "The complete genome of the hyperthermophilic bacterium Aquifex aeolicus.";
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-1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE
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-!- PATHMAX: PEPTIDOGLYCAN BIOSYMYHESIS.
-!- SUBCELLULAR LOCATION: CYTOPLASHIC (PROBABLE).
-!- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYIMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
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SEQUENCE 311 AA; 34569 MW; E27B65877EF65813 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              50.6%; Score 41; DB 1; 66.7%; Pred. No. 6.8;
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1; Mismatches
FERREDOXIN OXIDOREDUCTASE BETA SUBUNIT)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GAMMA CHAIN (BY SIMILARITY).
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                                                               Pyrococcus horikoshii.
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Best Local Similarity
Matches 8; Conserv
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SEQUENCE FROM N.A.
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30-MAY-2000 (Rel.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps
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-1- FUNCTION: CELL WALL FORMATION (BY SIMILARITY).

-1- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL-L-ALANINE - ADP + ORTHOPHOSPHATE + UDP-N-ACETYLMURAMOYL-L-ALANINE.

-1- PATHMAX: PEPTIDGLYCAN BIOSYNTHESIS.

-1- SUBCELLULAR LOCATION: CYTOPLASMIC (PROBABLE).

-1- SIMILARITY: BELONGS TO THE MURCDEF FAMILY.
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MEDLINE-20445173; PubMed-10993077;
Shigenobu S., Watanabe H., Hattori M., Sakaki Y., Ishikawa
"Genome sequence of the endocellular bacterial symbiont of
                                                                                                                                                                                       EMBL; AE000736; AAC07323.1; -.
InterPro; IPR000713; Mur_ligase.
Pfam; PF01225; Mur_ligase; 1.
Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding; Complete protecome.
NP_BIND 113 119 ATP (POTENTIAL).
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Peptidoglycan synthesis; Cell wall; Cell division; Ligase;
ATP-binding; Complete proteome.
NP_BIND 125 131 ATP (POTENTIAL).
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20-AUG-2001 (Rel. 40, Last annotation update)
UDP-N-ACETYLMURAMATE--ALANINE LIGASE (EC 6.3.2.8) (UDP-N-
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454 AA; 50893 MW; 12665EE14448232C CRC64;
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484 AA; 54311 MW; 06359D435D5590A7 CRC64;
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Bacteria; Proteobacteria; gamma subdivision; Buchnera.
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InterPro; IPR001064; Crystallin.
InterPro; IPR000713; Mur_ligase.
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Matches 7; Conservative
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(Rel. 40,
(Rel. 40,
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20-AUG-2001
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SEQUENCE
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MURC_BUCAIL

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MEDLINE-95324553; Pubmed=7601127;
Liger D., Masson A., Blanot D., van Heijenoort J., Parquet C.;
"Over-production, purification and properties of the uridine-diphosphate-N-acetylmuramate:L-alanine ligase from Escherichia coli.";
Eur. J. Blochem. 230, 800-87(1995).
-!- FUNCTION: CELL WALL FORMATION.
-!- CATALYTIC ACTIVITY: ATP + UDP-N-ACETYLMURAMOYL + L-ALANINE =
                                                   Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ikeda M., Wachi M., Jung H.K., Ishino F., Matsuhashi M.;
"Nucleotide sequence involving murG and murC in the mra gene cluster
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SYAIN-WIZ / MG1655;
MEDILINE-97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
Mau B., Shao Y.,
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Conditionally lethal Escherichia coli murein mutants contain point
defects that map to regions conserved among murein and folyl poly-
gamma-glutamate ligases: identification of a ligase superfamily.",
                                                                                                                                                                                                                                                                                                                                                     Escherichia coli.
Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae;
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                                                   ö
                  Length 484;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     "The complete genome sequence of Escherichia coll K-12.";
Science 277:1453-1474(1997).
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                                                                                                                                                                                                            MURC_ECOLI STANDARD; PRT; 491 AA.
191952; 007099;
01-NOV-1990 (Rel. 16, Created)
01-NOV-1990 (Rel. 19, Last sequence update)
01-AUG-1991 (Rel. 40, Last annoctation update)
UDD-N-ACETYLAMRAMATE-ALANNINE LIGASE (EC 6.3.2.8) (UDP-N-ACETYLMURAMYEL-ALANNINE SYNTHETASE).
                                                   4; Indels
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                50.6%; Score 41; DB 1; 57.1%; Pred. No. 11;
                                                   Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic Acids Res. 18:4014-4014(1990)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRAIN-CGSC 5988;
MEDLINE-97309380; PubMed-9166795;
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                                                   'n
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     region of Escherichia coli.";
                                                     Conservative
                                                                                     3 LLAALGYKVRASDM 16
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Query Match
Best Local Similarity
'-hag 8; Conserv?
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MURC_ECOLI
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Connor R., Churcher C.M., Barrell B.G., Rajandream M.A., Walsh S.V.;
Submitted (DEC-1995) to the EMBL/GenBank/DDBJ databases.
-: SUBCELLULAR LOCATION: INTECRAL MEMBRANE PROTEIN (POTENTIAL).
-: SIMILARITY: BELONGS TO THE AMINO ACID PERMEASE FAMILY.
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REMBL; X55034; CAA38668.1; -.

REMBL; D10483; BAA01356.1; -.

REMBL; AE000118; AAC13202.1; -.

REMBL; U67892; AAB60787.1; -..

REMBL; U67892; AAB6078.1; -..

RECGENE; EG10619; Mur_ligase.

RECGENE; REMBL; Complete proteome.

REMBL; U678925; Mur_ligase; L.

REMBL; U678925; L.

REMBL; U678925;
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53626 MW; D201B35931C013FB CRC64;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   01-FEB-1996 (Rel. 33, Created)
01-FEB-1996 (Rel. 33, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
PUTATIVE AMINO-ACID PERMEASE C11D3.08C.
SPACILD3.08C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pred. No. 11;
4; Mismatches
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PROSITE; PS00218; AMINO_ACID_PERMEASE_1; 1.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Schizosaccharomyces pombe (Fission yeast).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               InterPro; IPR002093; AA_rel_permease_1.
InterPro; IPR002027; Amino_acid_permease.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             50.6%;
50.0%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         8; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2 ELLAALGYKVRASDMA 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37 EVLANEGYQISGSDLA 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Schizosaccharomyces.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         491 AA;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match
Best Local Similarity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   NCBI_TaxID=4896
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Q10087;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               IF2 homolog in yeast.";
Science 280:1757-1760(1998).
-!- FUNCTION: FUNCTION IN GENERAL TRANSLATION INITIATION BY PROMOTING
THE BINDING OF THE FORMYLMETHIONINE-TRNA TO RIBOSOMES. SEEMS TO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SEQUENCE FROM N.A.
STRAIN=S28BC / AB972;
MEDLINE=59249563; PubMed=773198B;
Bussey H., Kaback D.B., Zhong W., Vo D.T., Clark M.W., Fortin N.,
Hall J., Ouellette B.F.F., Keng T., Barton A.B., Su Y., Davies C.K.,
                                                                                                                                                                                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Sutrave P., Shafer B.K., Strathern J.N., Hughes S.H.; "Isolation, identification and characterization of the FUN12 gene of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Choi S.K., Lee J.H., Zoll W.L., Merrick W.C., Dever T.E.; "Promotion of met-tRNAiMet binding to ribosomes by yIF2, a bacterial
                                                                                                                                                                                                                                                                                                                                                                                                                            Saccharomyces cerevisiae (Baker's yeast).
Eukaryota; Fungi; Ascomycota; Saccharomycotina; Saccharomycetes;
Saccharomycetales; Saccharomycetaceae; Saccharomyces.
                                                                                                                                                                                                   ô
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  'The nucleotide sequence of chromosome I from Saccharomyces
                                                                                                                                                                         Length 550;
                                                                                                                                                                                                   Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Submitted (APR-1996) to the EMBL/GenBank/DDBJ databases
                                                                                                                   POTENTIAL.
3DD1EF6003896E4C CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Proc. Natl. Acad. Sci. U.S.A. 92:3809-3813(1995)
                                                                                                                                                                         ï
                                                                                                                                                                                                                                                                                                                                                                       01-OCT-1996 (Rel. 34, Last sequence update)
15-DEC-1998 (Rel. 37, Last annotation update)
TRANSLATION INITIATION FACTOR IF-2.
                                                                                                                                                                        Score 41; DB 1
Pred. No. 12;
1; Mismatches
                                                                                                                                                                                                                                                                                                                              PRT; 1002 AA
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                    POTENTIAL.
POTENTIAL.
POTENTIAL.
                                                            POTENTIAL. POTENTIAL.
                                                                                        POTENTIAL. POTENTIAL.
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MEDLINE-94357438; Pubmed-8076820;
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201 221
346 266
93 303
6 406
406
473
5918 MW; 5
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                                                                                                                                                                        50.6%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Saccharomyces cerevisiae.";
Gene 146:209-213(1994).
                                                                                                                                                                                                   8; Conservative
                                                                                                                                                                                                                                                                                                                              STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    STRAIN-S288C / AB972;
                                                                                                                                                                      Query Match
Best Local Similarity
Matches 8; Conserv
                                                                                                                                                                                                                               1 DELLAALGYK 10
                                                                                                                                                                                                                                            32 DELLMSLGYK 41
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                                                                                                                                                                                                                                                                                                                                                                                                               YAL035W OR FUN12.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NCBI_TaxID=4932;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                cerevisiae.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Storms R.K.;
                                                                                                                                                                                                                                                                                                                           IF2P_YEAST
P39730;
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                    TRANSMEM
TRANSMEM
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IF2P_YEAST
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94 LLAAVDYKLKAS 105
                                    3 LLAALGYKVRAS 14
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01-FEB-1996
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   entities requires a license agreement (See http://www.isb-sib.ch/announce/
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Kawarabayasi Y., Sawada M., Horikawa H., Haikawa Y., Hino Y., Yamamoto S., Sakine M., Baba S.-I., Kosuqi H., Hosoyama A., Nagai Y., Sakai M., Ogura K., Otsuka R., Nakazawa H., Takamiya M., Ohfuku Y., Funahashi T., Tanaka T., Kudoh Y., Yamazaki J., Kushida N., Oguchi A., Aoki K.-I., Yoshizawa T., Nakamura Y., Robb F.T., Horikoshi K., Masuchi Y., Shizuya H., Kikuchi H.;
"Complete sequence and gene organization of the genome of a hyperthermophilic archaebacterium, Pyrococcus horikoshii OT3.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Archaea, Euryarchaeota, Thermococcales, Thermococcaceae; Pyrococcus.
NCBL_TaxID=53953;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               -1- SIMILARITY: BELONGS TO THE L5P FAMILY OF RIBOSOMAL PROTEINS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Score 41; DB 1; Length 1002; Pred. No. 22; 4; Mismatches 3; Indels
                                                                                                                                                                                                                                                                                                                                                                                       GTP (BY SIMILARITY).
W; 1A496195DAEIC283 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Probon; PD001076; Ribosomal_L5; 1.
PROSTTE; PS00358; RIBOSOMAL_L5; FALSE_NEG.
Ribosomal protein; Complete proteome.
SEQUENCE 188 AA; 21610 MW; 56CAP0BS053AECF4 CRC64;
                                                                                                                                                                                                                                                                                                                           Initiation factor; Protein biosynthesis; GTP-binding.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    15-DEC-1998 (Rel. 37, Created)
15-DEC-1998 (Rel. 37, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
50S RIBOSOMAL PROPEIN LSP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            188 AA.
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                                 or send an email to license@isb-sib.ch)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Interpro; IPR002132; Ribosomal_L5.
Pfam; PF00281; Ribosomal_L5; 1.
Pfam; PF00673; Ribosomal_L5_C; 1.
                                                                                         EMBL; U12980; AAC04996.1; -.
EMBL; L29389; AAA57228.1; ALT_SEQ.
EGD; SG000033; FUNI2.
InterPro; IPR000795; GTP_EFTU.
InterPro; IPR000178; IF2.
                                                                                                                                                                                                                                                                                                                                                         361 371 POL
412 419 GTF
1002 AA; 112268 MW;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         50.6%;
                                                                                                                                                                                                                           Interpro; IPR000178; IF2.
Pfam; PF00009; GTP_EFTU; 1.
Pfam; PF02131; IF2; 1.
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| 698 EVKAALGVKIAANDL 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ELLAALGYKVRASDM 16
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity
8; Conserve
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE FROM N.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RPL5P OR PH1765
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       RL5_PYRHO
AC 056431;
DT 15-DEC-1998
DT 15-DEC-1998
DT 15-DEC-1998
DT 20-AUG-2001
DE 50S RIBOSOM
GN RPL5P OR PH
CS Archaea; DO X NCBL_TAXID=
RN SEQUENCE FR
RX ARABILINE-993
RA YAMAMOLINE-993
RA YAMAMOLINE-993
RA YAMAMOLINE-993
RA YAMAMOLINE-993
RA AOKI K.-I.,
RA MASUCHI Y.,
RA AOKI K.-I.,
COMPLETE SWISS-CC
This SWISS-CC
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The European
CC C This SWISS-CC
C This SWISS-CC
C This SWISS-CC
C This FOOG
DR EMBL; APPOND
DR FFAM: PFOOG
DR FAMILS PEOOG
DR FAMILS PEOOG
DR FAMILS PEOOG
DR FAMILS PEOOG
DR PFAMI, 
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SEQUENCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps
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                                                                                                                                                                                                                                                                                                                                                                                       Happe B., Eltis L.D., Poth H., Hedderich R., Timmis K.N.; "Characterization of 2,2',3-trihydroxypiphenyl dioxygenase, an extradiol dioxygenase from the dibenzofuran- and dibenzo-p-dioxin-degrading bacterium Sphingomonas sp. strain RWI."; J. Bacteriol. 175:7313-7320(1993).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SIMILARITY: BELONGS TO THE EXTRADIOL RING-CLEAVAGE DIOXYGENASE
                                                                                                                                                                              Pseudomonas paucimobilis (Sphingomonas paucimobilis).
Bacteria; Proteobacteria; alpha subdivision; Sphingomonadaceae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ó
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
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NON (BY SIMILARITY).

E77B673329C87B32 CRC64;
                                              01-FEB-1996 (Rel. 33, Created)
30-MAY-2000 (Rel. 39, Last sequence update)
30-MAY-2000 (Rel. 39, Last annotation update)
2,2',3-TRIHYDROXYBIPHENYL DIOXYGENASE (EC 1.13.11.-).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Oxidoreductase; Dioxygenase; Aromatic hydrocarbons
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              IRON (BY SIMILARITY).
IRON (BY SIMILARITY).
293 AA.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ProDom; PD000977; Extradiol_dioxygnse; 1. PROSITE; PS00082; EXTRADIOL_DIOXYGENAS; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          InterPro; IPR000486; Extradiol_dioxygnse.
InterPro; IPR000325; Glyoxalase_1.
                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A., AND SEQUENCE OF 1-63
PRT;
                                                                                                                                                                                                                                                                                                                                                                  MEDLINE-94042906; PubMed-8226678;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             32146 MW;
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STANDARD;
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Matches 8; Conserva
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208
259
293 AA;
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NCBI_TaxID=13689;
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Gaps

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1; Indels

3; Mismatches

Conservative

Best_Local Similarity Matches 8; Conserv

Query Match

48.1%; Score 39; DB 1; Length 188; 66.7%; Pred. No. 9.2;

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J. Biol. Chem. 266:20928-20933(1991).
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                                                                                                                                                                                                                                                         ketisovalerate ferredoxin oxidoreductases from Pyrococcus furiosus and pyruvate ferredoxin oxidoreductase from Thermotoga maritima."; J. Bacteriol. 178:248-257(1996).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
                                                                                                                                                               Archaea; Euryarchaeota; Thermococcales; Thermococcaceae; Pyrococcus.
NCBL_TaxID-2261;
                                                                                  30-MAY-2000 (Rel. 39, Last sequence update)
V-AAY-2000 (Rel. 39, Last annotation update)
KETOISOVALERATE OXIDOREDUCTASE SUBUNIT VORB (EC 1.....) (VOR) (2-OXISOVALERATE OXIDOREDUCTASE BETA CHAIN) (2-OXOISOVALERATE-
WORD OXIDOREDUCTASE BETA SUBUNIT).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Bacteria; Proteobacteria; gamma subdivision; Enterobacteriaceae,
                                                                                                                                                                                                                                    Kletzin A., Adams M.W.A.; "Molecular and phylogenetic characterization of pyruvate and 2-
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Furuchi T., Kashiwagi K., Kobayashi H., Igarashi K.; "Characteristics of the gene for a spermidine and putrescine transport system that maps at 15 min on the Escherichia coli chromosome.";
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           48.1%; Score 39; DB 1; Length 311; 58.3%; Pred. No. 15;
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01-NOV-1991 (Rel. 20, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SPERMIDIAE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA.
POTA OR B1126 OR Z1831 OR ECS1571.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  3; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                          311 AA; 34766 MW; 07CC02452E3C6074 CRC64;
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                                                       311 AA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 2; Mismatches
                                                                                                                                                                                                    SEQUENCE FROM N.A., AND SEQUENCE OF 1-7
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDLINE-92041956; PubMed-1939142;
                                                                                                                                                                                                               STRAIN=DSM 3638;
MEDLINE=96125254; PubMed=8550425;
                                                                           30-MAY-2000 (Rel. 39, Created)
                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; X85250; CAA59503.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Escherichia coli, and Escherichia coli 0157:H7.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Best Local Similarity 58.3
Matches 7; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STANDARD;
                                                       STANDARD;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NCBI_TaxID=562, 83334;
 61 LAAIGWNVDPSDLA 74
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90 LKAMGYKVKGED 101
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                                                                                                                                                       Pyrococcus furiosus
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SEQUENCE 311
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                                                      VORB PYRFU
Q51802;
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                                RESULT 13
VORB_PYRFU
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POTA_ECOLI
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MEDLINE-21156231; PubMed=11258796;
Hayashi T., Makino K., Ohnishi M., Kurokawa K., Ishii K., Yokoyama K., Han C.-G., Ohtsubo E., Nakayama K., Murata T., Tanaka M., Tobe T., Iida T., Takami H., Honda T., Sasakawa C., Ogasawara N., Yasunaga T., Kuhara S., Shiba T., Hattori M., Shinagawa H.;
"Complete genome sequence of enterohemorrhagic Escherichia coli 0157:H7 and genomic comparison with a laboratory strain K-17".
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Oshima T., Aiba H., Baba T., Fujita K., Hayashi K., Honjo A.,
Ikemoto K., Inada T., Itoh T., Kajihara M., Kanai K., Kashimoto K.,
Kimura S., Kitagawa M., Makino K., Masuda S., Miki T., Mizobuchi K.,
Mori H., Motomura K., Nakamura Y., Nashimoto H., Nishio Y., Sampel G., Seki Y., Tagami H., Takemoto K., Wada C., Yamamoto Y.,
Yano M., Horiuchi T.;
"A 718-kb DNA sequence of the Escherichia coli K-12 genome
corresponding to the 127-28.0 min region on the linkage map.";
SEQUENCE FROM N.A.
STRAIN=K12 / MG1655;
MEDLINE=97426617; PubMed-9278503;
Blattner F.R., Plunkett G. III, Bloch C.A., Perna N.T., Burland V.,
Riley M., Collado-Vides J., Glasner J.D., Rode C.K., Mayhew G.F.,
Gregor J., Davis N.W., Kirkpatrick H.A., Goeden M.A., Rose D.J.,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SEQUENCE FROM N.A.

STRAIN=0157:H7 / EDL933 / ATCC 700927;

MEDLINE-21074935. PubMed-11206551;

Perna N.T., Plunkett G. III, Burland V., Mau B., Glasner J.D.,

Rose D.J., Mayhew G.F., Evans P.S., Gregor J., Kirkpatrick H.A.,

Posfai G., Hackett J., Klink S., Boutin A., Shao Y., Miller L.,

Grotbeck E.J., Davis N.W., Lim A., Dimalanta E.T., Potamousis K.,

Apodaca J., Anantharaman T.S., Lin J., Yen G., Schwartz D.C.,

Welch R.A., Blattner F.R.;

"Genome sequence of enterohaemorrhagic Escherichia coli 0157:H7.";
                                                                                                                                                                                                                                                                      "The complete genome sequence of Escherichia coli K-12."; Science 277:1453-1474(1997).
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InterPro; IPR003593; AAA.
InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
                                                                                                                                                                                                                                                                                                                                                                                                                             STRAIN-K12;
MEDLINE-97061202; PubMed-8905232;
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EMBL; ABC00212; AAC74210.1; -.
EMBL; D90747; BAA35946.1; -.
EMBL; D90748; BAA35948.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EMBL; AE005326; AAG55930.1; -. EMBL; AP002555; BAB34994.1; -.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nature 409:529-533(2001).
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                                                                                                                                                                                                                                                                                                                                                                                     SEQUENCE FROM N.A.
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                                                                                                                                                                                                                                          Mau B., Shao Y.;
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                                                                                                                                                                                                                                                                                                                                                                            Gaps
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                                                                                                                                                                                                                                                                                                                                   Bacteria; Proteobacteria; gamma subdivision; Pasteurellaceae;
Pfam; PFUUUUJ; AAA; 1.
SWART; SW00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
Transport; ATP-binding; Inner membrane; Complete proteome.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Transport, ATP-binding, Inner membrane; Complete proteome. NP_BIND 52 59 ATP (POTENTIAL). SEQUENCE 381 AA; 43429 WW; 3E61DD3D062EBECA CRC64;
                                                                                                  Length 378
                                                                                                                                                                                                                                                                       01-NOV-1995 (Rel. 32, Last sequence update)
20-AUG-2001 (Rel. 40, Last annotation update)
SPERMIDINE/PUTRESCINE TRANSPORT ATP-BINDING PROTEIN POTA.
                                                                                                                          2; Indels
                                                                                                  DB 1;
19;
                                                                                                                                                                                                                                    381 AA
                                                                                                                         2; Mismatches
                                                                                                  48.1%; Score 39; 66.7%; Pred. No.
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InterPro; IPR003439; ABC_transportr.
InterPro; IPR001687; ATP_GTP_A.
Pfam; PF00005; ABC_tran; 1.
SMART; SM00382; AAA; 1.
PROSITE; PS00211; ABC_TRANSPORTER; 1.
                                                                                                                                                                                                                                    PRT;
                                                                                                                                                                                                                                                            Created)
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                                                                                                             Best Local Similarity 66.7
Matches 8; Conservative
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                                                                                                                                                                                                                                                                                                                      Haemophilus influenzae.
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01-NOV-1995 (
20-AUG-2001 (
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P45171;
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      Query Match
      48.1%; Score 39; DB 1; Length 381;

      Best Local Similarity 66.7%; Pred. No. 19;

      Matches 8; Conservative 2; Mismatches 2; Indels 0; Gaps 0;

      Qy 1 DELLAALGYKVR 12

      Db 174 DESLSALDYKLR 185
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Search completed: December 19, 2001, 17:10:29 Job time: 175 sec

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Sequence:

Searched:

Database

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Q9enKS porcine rep
Q9enKS porcine rep
Q98aN9 porcine rep
Q99aN5 porcine rep
Q9dln9 porcine rep
Q9dln9 porcine rep
Q9dln8 porcine rep
Q9476 arabidopsis
Q9sal7 arabidopsis
Q9sal7 arabidopsis
Q9ywd2 neisseria mi
Q9ywd2 neisseria m
Q9jwd2 neisseria m
Q9jx2 peudomonas
Q9ic503 lactate deh
Q9ic503 lactate deh
Q9ic503 peudomonas
Q9lc50 pseudomonas
Q9lc50 pseudomonas
Q9lwC5 pseudomonas
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Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Pooideae;
Triticeae; Triticum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       [1]
SEQUENCE FROM N.A.
MEDILINE-99347734; PubMed=10421366;
Peng J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M.,
Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F.,
Sudhakar D., Christou P., Snape J. W., Gale M.D., Harberd N.P.;
"'Green revolution' genes encode mutant gibberellin response
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                                      0917c0
09enk5
09e8m9
099bu5
099av5
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modulators.";
Nature 400:256-261(1999).
BMBL; AJ242531; CAB51555.1; -.
EMBL; AJ242531; CAB51555.1; -.
TOTAL 623 AA; 65337 MW; F2BAC34996D0A84F CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-UN-2001 (TrEMBLrel. 17, Last annotation update)
GIBBERELLIN RESPONSE MODULATOR.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Q9MB96;
01-OCT-2000 (TrEMBLrel. 15, Created)
01-OCT-2000 (TrEMBLrel. 15, Last sequence update)
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                                                                                                                                                                                                                                                                                                                                                                     291528
291577
206503
2916C5
2912R2
2992R80
                   Q9YN01
Q9J7C0
Q9ENK5
Q9E8M9
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09DLN9
09DLP1
09DLP0
09DLN8
080476
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Q9YAH8
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Q30707
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Q9RGR6
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Ogst48 zea mays (m

Ogst48 zeabidopsis

Ogjf53 arabidopsis

Ogjf43 arabidopsis

Ogjf44 arabidopsis

Ogjf48 arabidopsis

Ogsrp9 arabidopsis

Ogsrp9 arabidopsis

Ogslp3 arabidopsis
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09wjb3 porcine rep
09wbq4 porcine rep
                                                                                                                                                               (without alignments)
108.256 Million cell updates/sec
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                                                                                                                                           ; Search time 22.97 Seconds
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                     GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd
                                                                                                                                                                                                                                                                                                                                                                                                                Total number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                                                                         473505 seqs, 146272329 residues
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Maximum Match 100%
Listing first 45 summaries

    protein search, using sw model

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Q9MB96
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Gapop 10.0 , Gapext 0.5
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sp_invertebrate:*
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sp_vertebrate:*
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sp_bacteria:*
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Result

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us-09-485-529-104.rspt

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Theologis A., Ecker J.R., Palma C.J., Federspiel N.A., Kaul S.,

Theologis A., Cara A., Altafi H., Araujo R., Bowman C.L., Brooks S.Y.,

Banchler E., Chan A., Chao O., Chen H., Cheuk R.F., Chin C.W.,

A Chung M.K., Conn L., Conway A.B., Conway A.B., Creasy T.H., Dewar K.,

A chung W.K., Conn L., Conway A.B., Creasy T.H., Dewar K.,

A chun P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A chun P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A chun P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A chun P., Etgu P., Feldblyum T.V., Feng J.-D., Fong B., Fujii C.Y.,

A chun F., Coldsmith A.D., Haas B., Hansen N.F., Hughes B., Huzar L.,

A there J.L., Jenkins J., Johnson-Hopson C., Khaykin E.,

A the C.J., Koo H.L., Kremenetskaia I., Kurtz D.B., Kwan A., Lam B.,

A Lin X., Liu S.X., Liu Z.A., Lucos J.S., Malti R., Marziali A.,

A Lin X., Liu S.X., Liu Z.A., Lucos J.S., Malti R., Marziali A.,

A sakano H., Salzerg S.L., Schwartz J.R., Shinn P., Southwick A.M.,

A Sakano H., Zallon L.J., Tambunga G., Toriuni M.J., Town C.D.,

W Uterback T., Van Aken S., Vaysberg M., Vysotskaia V.S., Walker M.,

A "Sequence and analysis of chromosome I of the plant Arabidopsis
                                      Bukaryots thallana (Mouse-ear cress).
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Vizidiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnollophyta; eudicotyledons; core eudicots; Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE FROM N.A.
Sato S., Nakamura Y., Kaneko T., Kato T., Asamizu E., Kotani H.,
Tabata S., Mewes H.W., Rudd S., Lemcke K., Mayer K.F.X.;
Submitted (ANG-2000) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length 523;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length 511;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             2; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        EU Arabidopsis sequencing project;
Submitted (AUG-2000) to the EMBL/GenBank/DDBJ databases.
EMBL; AIJ91150; CACO1893.1; - OF6CE0BD13403C35 CRC64;
SEQUENCE 523 AA, 57326 WW; OF6CE0BD13403C35 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Nature 408:816-820(2000).
EMBL; AC020665; AAG52171.1; -.
SEQUENCE 511 AA; 56754 MW; 1E60071697C92A9F CRC64;
  01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
GIBBERELLIN REGULATORY PROTEIN, PUTATIVE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Created)
Last sequence update)
Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 70; DB 10;
Pred. No. 0.0013;
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Pred. No. 0.0014;
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Arabidopsis thaliana (Mouse-ear cress).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRT;
                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. COLUMBIA;
MEDLINE-21016719; PubMed-11130712;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.4%;
82.4%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      86.48;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           82.48;
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Best Local Similarity 82.4
Matches 14; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRELIMINARY;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
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Q9LF53
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade;
Panicoideae; Andropogoneae; Zea.
NCBI_TaxID=4577;
                                                                                                                                                                                                                                                            Ogawa M., Kusano T., Katsumi M., Sano H.;
"Rice gibberellin-insensitive gene homolog, OsGAI, encodes a nuclear-
localized protein capable of gene activation at transcriptional
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
                                                        Oryza sativa (Rice).
Oryza sativa (Ridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE FROM N.A.
MEDLINE=99347734; PubMed=10421366;
MEDLINE=99347734; PubMed=10421366;
Mend J., Richards D.E., Hartley N.M., Murphy G.P., Devos K.M., Flintham J.E., Beales J., Fish L.J., Worland A.J., Pelica F., Sudhakar D., Christou P., Snape J.W., Gale M.D., Harberd N.P., "Green revolution' genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ;
0
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Pred. No. 7.2e-05;
Mismatches 0; Indels
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                                                                                                                                                                                                                                                                                                                                               Gene 245:21-29(2000).
EMBL; AB030956; BAA90749.1; -.
SEQUENCE 625 AA; 65406 MW; 034FF02719D42E97 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       630 AA; 66028 MW; 3D56851726C51042 CRC64;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              01-MAY-2000 (TrEMBLrel. 13, Created)
01-MAY-2000 (TrEMBLrel. 13, Last sequence update)
01-MAY-2001 (TrEMBLrel. 16, Last annotation update)
GIBBERELLIN RESPONSE MODULATOR (FRAGMENT).
01-OCT-2000 (TrEMBLrel. 15, Last annotation update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    01-JUN-2001 (TrEMBLrel. 17, Created)
01-JUN-2001 (TrEMBLrel. 17, Last sequence update)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Score 78; DB 10; I
Pred. No. 7.3e-05;
.; Mismatches 0;
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                                                                                                                                                                                          SEQUENCE FROM N.A.
STRAIN-CV. NIPPONBARE;
MEDLINE-20179680; Pubmed-10713441;
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EMBL; AJ242530; CAB51557.1; -.
NON_TER 630 630
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94.1%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                             96.3%;
94.1%;
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Best Local Similarity
Matches 16; Conserv
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Matches 16; Conser
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SEQUENCE
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Q9C8Y3;
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RESULT STATES STATES

RESULT 09C8Y3

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Gaps

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Cheur R., Shin P., Brooks S., Buehler E., Chao Q., Johnson-Hopson C., Khan S., Kim C., Altafi H., Bei B., Chin C., Chiou J., Choi E., Conn L., Conway A., Gonzalez A., Hansen N., Howing B., Koo T., Lam B., Lee J., Lenz C., Li J., Liu A., Liu J., Liu S., Mukharsky N., Nguyen M., Palm C., Pham P., Sakano H., Schwartz J., Southwick A., Theologis A., Ecker J., The Embl. Gons B., Cooker J., Submitted (JUN-2000) to the Embl./GenBank/DDbJ databases.

Submitted (JUN-2000) to the Embl./GenBank/DDbJ databases.

Embl. AC006917, AAF79228 I; SEQUENCE 533 AA; 58926 MW; 6464B8C129D79528 CRC64;
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82.4%; Pred. No. 0.0014;
Live 2; Mismatches 1; Indels
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MEDLINE-9801192; PubMed=9389651;
MEDLINE-9801192; PubMed=9389651;
MEDLINE-9801192; PubMed=9389651;
MURPHY G.P., Harbard N.P.;
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Genes Dev. 11:3194-3205(1997).
EMBL; Y15193; CAA75492.1; ---
Mendel; 24070; Arath;3051;24070.
SEQUENCE 532 AA; 58789 MW; 4AF4BC6EC4265503 CRC64;
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Truong H.N., Caboche M., Daniel-Vedele F.;
"Sequence and characterization of two Arabidopsis thaliana cDNAs
isolated by functional complementation of a yeast gln3 gdh1 mutant.";
FEBS Lett. 410:213-218(1997).
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Bukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae,
eurosids II; Brassicales, Brassicaceae, Arabidopsis.
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Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta:
Spermatophyta: Magnoliophyta; eudicotyledons; core eudicots: Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
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Mendel; 24146; Arath;3051;24146.
SEQUENCE 532 AA; 58789 MW; 17AC719CA8072239 CRC64;
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
NCBI_TaxID=3702;
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LIN X., KRAUL S., Town C.D., Benito M., Creasy T.H., Haas B.,
Ronning C.M., Koo H., Fujii C.Y., Utterback T.R., Barnstead M.E.,
Bowman C.L., White O., Nierman W.C., Fraser C.M.;
"Arabidopsis thaliana chromosome III BAC T21P5 genomic sequence.";
Submitted (OCT-1999) to the EMBL/GenBank/DDBJ databases.
EMBL; AC009895; AaR01590.1; -.
SEQUENCE 547 AA; 60493 MW; C4D18D5951D95634 CRC64;
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Truong H.N., Caboche M., Daniel-Vedele F.;
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STRAIN-CV. COLUMBIA;

MEDLINE-20083487; PubMed-10617197;

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Lin X., Kaul S., Rounsley S.D., Shea T.P., Benito M.-I., Town C.D.,

Fujii C.Y., Mason T.M., Bowman C.L., Barnstead M.E., Feldblyum T.V.,

Buell C.R., Ketchum K.A., Lee J.J., Ronning C.M., Koo H., Mcffat K.S.,

Gronin L.A., Shen M., VanAken S.E., Umayam L., Tallon L.J., Gill J.E.,

Adams M.D., Carrera A.J., Creasy T.H., Goodman H.M., Somerville C.R.,

Copenhaver G.P., Preuss D., Nierman W.C., White O., Elsen J.A.,

Salzberg S.L., Fraser C.M., Venter J.C.;

Sequence and analysis of chromosome II of Arabidopsis thallana.";
Arabidopsis thaliana (Mouse-ear cress).
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana (Mouse-ear cress).
Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae;
eurosids II; Brassicales; Brassicaceae; Arabidopsis.
                                                                                                                                                                                                                                                                                                                                       Gaps
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EMBL; AC005560; AAC67333.1; -.
SEQUENCE 587 AA; 64035 MW; FC92E7F9408072AA CRC64;
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AT2G01570.
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Last sequence update)
Last annotation update)
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ORFRM1 DNA.
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                                                            "Cloning of the Arabidopsis thaliana RGA-like gene, a putative member of the VHIID domain transcription factor family.";
submitted (MAR-1998) to the EMBL/GenBank/DDBJ databases.
EMBL, AJ22457; CAA12242.1;
Mendel: 29006, Arath,3051,29006.
InterPro: IRR001680; WD40.
InterPro: PR001080; WD40.1.
PR0NITE; PS50082; WD_REPEATS_2; 1.
PROSITE; PS50082; WD_REPEATS_2; 1.
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Fubuta M., Inazawa J., Torli T., Tsuzuki K., Shimada E., Habuchi O.;
"Moolecular cloning and characterization of human keratan sulfate
Gal-6-sulfotransferase."
J. Biol. Chem. 272:32321-32328(1997).
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Eukaryota; Metazoa; Chordata; Craniata; Vertebrata; Euteleostomi;
Mammalia; Eutheria; Primates; Catarrhini; Hominidae; Homo.
  Sanchez-Fernandez R., Ardiles-Diaz W., van Montagu M., Inze D., May M.J.;
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MEDLINE-99168906; PubMed-10049591;
Li X., Tedder T.F.;
"CHST1 and CHST2 sulfotransferases expressed by human vascular endothelial cells: cDNA cloning, expression, and chromosomal
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Pred. No. 0.0018;
1; Mismatches 2; Indels
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Submitted (JUL-1996) to the EMBL/GenBank/DDBJ databases.
                                                                                                                                                                                                                                                                                                                Repeat; WD repeat.
SEQUENCE 662 AA; 73126 MW; 958AB73D42121CA8 CRC64;
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01-JUN-1998 (TrEMBLrel. 06, Last sequence update)
01-MAY-1999 (TrEMBLrel. 10, Last annotation update)
CHONDROITIN-6-SULFOTRANSFERASE.
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Curr. Opin. Lipidol. 7:0-0(1996).
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Genomics 55:345.347(1999).
EMBL; UG5637; AAC28776.1; -.
EMBL; AB003791; BAA24840.1; -.
EMBL; AF090137; AAD19878.1; -.
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Best Local Similarity 82.4%;
Matches 14; Conservative
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Marasco R., Varcamonti M., Ricca E., Sacco M.;
"A new Bacillus subtilis gene with homology to Escherichia coli prc.";
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DB 4; Length 411; 27;
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01-NOV-1996 (TrEMBLrel. 01, Last sequence update)
01-JUN-2001 (TrEMBLrel. 17, Last annotation update)
                                                                                                                                                                                                                                                                                                                             Bacteria; Firmicutes; Bacillus/Clostridium group; Bacillus/Staphylococcus group; Bacillus.
NCBI_TaxID=1423;
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Pred. No. 32;
4; Mismatches
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                                    4; Mismatches
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Score 44;
Pred. No. 2
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EMBL; X98341; CAA66987.1; -.
InterPro; IPR001478; PD2.
InterPro; IPR003581; TSPC.
Pfam; PF00595; PD2; 1.
PROSITE; PS50106; PD2; 1.
54.3%;
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SMART; SM00245; TSPC; 1
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1 (bases 1 to 51)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development Patent; WO 9909174-A 105 25-FEB-1999; HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers

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                  Description
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Sequence 105 from Patent WO9909174.
AX005896
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                GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
                                                                                                                                                                                                                                                                                                                                                       tal number of hits satisfying chosen parameters:
                                                                                                                                                                                                                                                                                                                  1472140 seqs, 8248589755 residues
                                                                                                                       December 19, 2001, 17:30:48
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Maximum Match 100%
Listing first 45 summaries
                                                                                    nucleic - nucleic search, using sw model
                                                                                                                                                                                                                                                                 IDENTITY_NUC Gapop 10.0 , Gapext 1.0
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em_htgo_inv:*
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278205 Bovine herp

24-AUG-2000

/organism="Triticum aestivum"

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/organism="Triticum aestivum"
/db_xref="taxon:4565"
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Sequence 14 from Patent WO9909174.
AX005805
                                                                                    modulators
Nature 400 (6741), 256-261 (1999)
                                                                                                                                                                                                                                                                                                                                                                        /gene="rht-Dla"
/note="GAI ortholog"
/codon_start=1
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Spermatophyta; Magnollophyta; Lillopsida; Poales; Poaceae;
Triticum.

1 (bases 1 to 453)
Harberd, N. P. and Peng, J.
Genetic control of plant growth and development
Patent: WO'9909174-A 66 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TAE242531 1872 bp DNA PLN 28-JUL-1999
Triticum aestivum rht-Dla gene for gibberellin response modulator.
AJ242531
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
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gibberellin response modulator; rht-Dla gene.
bread wheat.
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                                                                      Query Match 100.0%; Score 51; DB 6; I
Best Local Similarity 100.0%; Pred. No. 0.00015;
Matches 51; Conservative 0; Mismatches 0;
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lilarity 100.0%; Pred. No. 7.8e-05;
Conservative 0; Mismatches 0;
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/db_xref="taxon:4565"
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             7
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AX005857
AX005857.1 GI:9928852
/db_xref="taxon:4565"
7 a 16 c 21 q
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ALPVYVVDTQEAGIRLVHALLACAEAVQQENLSAAEALVKQIPLLAASQGGAMRKVAA
YFGEALARRVFRFRPQPDSSLLDAAFADLLHAHFYESCPYLKFAHFTANQAILEAFAG
CRRVHVVDFGIKQGMQMPALLQALALRPGGPPSFRLTGVGPPQPDETDALQQVGWKLA
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GELEKULGYRAVRANPRALVYVEQEANINISGTFLEDFFPESLHYYSTMFDSLEGSSGGG
PSEVSSGAARAARAARAARATDVYNSEEVILGEGOOTONVACEGAERTERHETLAGWRRILGNA
GFETVHLGSNAYKQASTLLALFAGGGGGYKVEEKEGCLTLGWHTRPLIATSAWRLAGP
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1 (bases 1 to 2125)
Harberd, N.P. and Peng, J.
Facebette control of plant growth and development
Patent: WO 990174-A 14 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Pooldeae; Triticeae; Triticum.

1 (bases 1 to 1872)

Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M.,
Flintham,J.E., Beales,J., Fish,L.J., Worland,A.J., Pelica,F.,
Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P.
Green revolution' genes encode mutant gibberellin response
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3. (bases 1 to 1872)
Richards, D. E.
Direct Submission
Submitted (25-MAY-1999) Richards D. E., Molecular Genetics, John Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps
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Harberd, N.P., Peng, J. and Richards, D.E.
Green revolution genes encode mutant gibberellin response
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /product="gibberellin response modulator"
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bread wheat.
Triticum aestivum
Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooideae; Triticeae, Triticum.
1 (bases 1 to 324)
Harberd, N. P. and Peng, J.
Harberd, N. P. and Peng, J.
Harberd, W. 9909174-A 76 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
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Best Local Similarity 100.0%; Pred. No. 4.5e-05;
Matches 51; Conservative 0; Mismatches 0;
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Pred. No. 0.00032;
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141 c 85 g 56 t
   /note="n is any nucleotide"
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1940
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2681
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Sequence 76 from Patent WO9909174.
                             /note="n is any
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Tritlceae; Tritlcum.

E 1 (bases 1 to 2709)
S Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Lorentic Control of plant growth and development
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualifiers
1. 2709
/db_xref="taxon:4555"
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                                                                                                                                                                                                     139 GACGAGCTGCTGGCGGCGCTCCGGGTACAAGGTGCGCGCCTCCGACATGGCG 189
                                                                                                                           Length 2125
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                                                                                                                        ch 100.0%; Score 51; DB 6; 1
1 Similarity 100.0%; Pred. No. 4.8e-05;
51; Conservative 0; Mismatches 0;
Location/Qualifiers
1. 2125
/organism="Triticum aestivum"
/db_xref="taxon:4565"
1 768 c 723 g 309 t
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Sequence 3 from Patent W09909174.
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LGYKVRSSDMADVAQKLEQLEMAMGMGGVSAPGAADDGFVSHLATDTVHYNPSDLSSW
VESMLSELNAPLPPIPPAPPARHASTSSTVTGGGGSGFFELPAAADSSSSTYALRPI
SLPVVATADPSAADSARDTKRMRTGGGSTSSSSSSSSSLGGGASRGSVVEAAPPATQG
                                                                                                                                                                                                                                                                        AAAANAPAVEVVVOTQEAGIRLVHALLACAEAVOOENFAAAEALVKOIPTLAASQGG
AMRKVAAYFECELARRVYRFRERDSTULDAAFADLUHAHFESGEYLKREHFTHAQAI
LEAFAGCHRVHVDDEGIKQGMQWPALLALRPGGEPSFRLTGVGPPOPDETDALQO
VGWKLAQCAHTIRVDFQYRGLVAATLADLEPPMLQPEGEADANEEPEVIAVNSVFELH
                                                                                                                                                                                                                                                                                                                                                   RLLAQPGALEKVLGTVHAVRPRIVTVVEQEANHNSGSFLDRFTESLHYYSTMFDSLEG
GSSGQAELSPPAAGGGGGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQWRNRLG
RAGFEPVHLGSNAYKQASTLLALFAGGDGYRVEEKEGCLTLGWHTRPLIATSAWRVAA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Sherhartoideae; Oryzeae; Oryzea.

1 (bases 1 to 122497)

Buell, C.R., Yuan, Q., Ouyang, S., Moffat, K.S., Hill, J.N., Shartsbeyn, M., Burgass, S., Hance, M., Shvartsbeyn, M., Tsitrin, T., Riggs, F., Hislao, J., Zismann, V., Blunt, S., Pal, G., VanAken, S.E., Utterback, T.R., Feldblyum, T.V., Quackenbush, J., Salzberg, S.L., White, O. and Fraser, C.M.
Oryza sativa chronosome 3 BAC OSJNBb0022E02 genomic sequence Unpublished
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Direct Submission
Submitted (25-JAN-2001) The Institute for Genomic Research, 9712
Medical Center Dr. Rockville, MD 20850, USA
3 (bases 1 to 122497)
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Medical Center Dr, Rockville, MD 20850, USA
4 (bases 1 to 122497)
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Submitted (03-MAY-2001) The Institute for Genomic Research, 9
Medical Center Dr. Rockville, MD 20850, USA, rbuell@tigr.org
On Apr 20, 2001 this sequence version replaced gi:13605985.
Address all correspondence to:rice@tigr.org
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Pred. No. 0.002;
0; Mismatches
'dev_stage="seedling"
                                                                                                                                                                                                                                                                                                                                                                                                                                  771 g
                                                                                               /note="GAI homolog'
                                                                                                                                        /product="OsGAI"
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                                                                             /gene="OsGAI"
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Best Local Similarity 94.0%;
Matches 47; Conservative C
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1 (Dases 1 to 770)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 12 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
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Mikihiro Ogawa, Nara Institute of Science and Technology, Plant
Molecular Breeding: Takayama 8916-5, Ikoma, Nara 630-0101, Japan
(E-mail:m-Ogawa@bs.aist-nara.ac.jp, Tel:+81-743-72-5652,
    Gaps
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Rice gibberellin-insensitive gene homolog, OsGAI, encodes a
nuclear-localized protein capable of gene activation at
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
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                                        DB 6; Length 770;
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  2; Indels
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Oryza sativa mRNA for OsGAI, complete cds.
AB030956
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Pred. No. 0.0029;
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Squence 12 from Patent W09909174.
AX005803.1 GI:9928800
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/db_xref="taxon:4530"
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
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Gene 245 (1), 21-29 (2000)
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.15274,15344. .16687,16818. .17803,
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/gene="OSJNBb00022E02.12"
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IVGSKCHSCVOSKOPRPHKAAEERNIAPLELLHSDLCEMNGVLTKGGRRYFFTLID
DATRECYVLLKTKDEALDYFKIYKAEPENULDRY IKRLASDRGGEFFSNEFDLFCEE
HGIIHERTPPYSPESNGIAERNRTJTDLVNAMLDTAGLPKAMMGEALLTSNHYLNR
PNRNKDKTPYEIWIGRKPSLSYLRTWGCLAKVNVPTTKRKLGPKTVDCVFLGYAHHS
TARFLIVKSEVPDMHVGTTIMESRDAFFESFFPMKDTHSGSNQPSEIIPSGTAHHS
TEHTHELVSEEDVSRAPRKSRRORTAKSRGDDFTVTUVDDTPKSISAYASPDADVNR
EAVRSEMDSIIANGTWEVTERPYGCKPVGCKWVFKKLRPDASHGLLVHQMDVKTAFI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NGELDEEIYMDQPDGFVVEGQEGKVCKLLKSLYGLKQAPKQMHEKFDKTLTSAGFAVN
EADKCVYYRHGGGGGVILCLYVDDILIFGTNLEVINEVKSFLSQNFDMKDLGVADVIL
NIKLIRGENGITLLQSHYVEKILNRFGYIDSKPSPTPYDPSLLLRKNKRIARNQLEYS
                                                                                                                                    RVKSKPTVDLKIVFLPLLAFEVIILADNFRMCRALMPGDEESMSDEAIWETLPHFWVA
ISMVFLIAATTFTLLKLSGDVGALGWMDLFINYGIAECFAFLVCTRWFNPMIHKSPNP
GEASSSSAAIRYRDWESGLLLPSLEDHEQERLCGLPDIGGHVMKIPLVIFQVLLCMRL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /translation="MAGFADALRPDKFTGVHFKRWQIRVTLWIJAMKCFWVSTGKPEG
VLTAEQQKQFEEATTLFVGCILSVLGDRLVEVYMHMTDAKELMDALNTKFGATDASND
LYIMEQFHDYKMADNRSVVEQAHEIQTMAKELELLKCVLPDKFVAGCIIAKLPPSWRS
                                                                                                                                                                                                                               EGTPPSAQYIPIFALFSPLFILGGAGYLFSLARLLEKVYLLLRNGPVSPNYLTISSKY
RDCFAFLHRGSRLLGWWSIDEGSKEEQARLFYTESTGYNTFCGYPPEVVRKMPKRDLA
EEVWRLQAALGEQSEITKCTKQEFERLQNEKVLCRICYEGEICMVLLPCRHRTLCKTC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FGTALKHKRQEYSVEGLIASLDVEEKAREKDAASKGDGGOSSANVVHKAQNKSKGKYK
AQQTTNFKKQKKNNNNPNQDERTCFVCGQVGHLARKCPQRKGMKAPAGQTSKSANVTI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     QIIGSLMYLASATRPDISFAVSKLSRFTSNPGDDHWRALERVMRYLKGTVELGLHYTG
YPAVLEGYSDSNWISDVDEIKATSGYVFTLGGGAVSWRSCKQTILTRSTWEAELFALD
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TITKCDRQCIEGDGFETHSILEGTHLCELDCWSQSMKILGESSRKLTKDLGV"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            GNTGDGSGYGRTGFHRPNGEWVTCFCSWCWHGRSEVYFGKDRAAEERAACPFYRQESC
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /gene="OSJNBb0022E02.12"
/note="similar to gag pol polyprotein GB:AAD12997
GI:4234852 (2ea mays)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /product="putative gag-pol polyprotein"
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                                                                                                                                                                                                                                                                                                                                                                                        /rpt_family="(CGGGGG)n"

complement(12558. 12580)

/rpt_family="(GA)n"

/oin(<14168. 15023,15131. 152)

17887. 18048, 18262. >18366)
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                                                                                                                                                                                                                                                                                                                              SDKCKKCPICRVPIEERMPVYDV" complement(12328. .12420)
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complement(20459. .20487)
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complement(22544. .22588)
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21271. .21576
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                                                                                    Genes were identified by a combination of several methods: Gene prediction programs including Fgenesh (http://www.softberry.com/), genscan and Genescan+ (Chris Burge, http://www.softberry.com/), http://CRR-081.mit.edu/GENSCAN.html), GeneMarkHWM (Mark Borodovsky, http://genemark.biology.gatech.edu/GeneMark/), and GeneSplicer (Mihaela Pertea and Steven Salzberg, contact mperteaetigr.cog/, searches of the complete sequence against a peptide database and the plant EST database at TIGR (http://www.tigr.org/tdb/tg1.shtml). Annotated genes are named to indicate the level of evidence for their annotation. Genes without significant peptide similarity to other proteins are named similarity but with EST similarity are named as unknown proteins. Genes without protein or EST similarity, that are predicted by more than two gene prediction programs over most of their length are annotated as hypothetical proteins. Genes encoding tRNAs are predicted by tRNAscan-SE (Sean Eddy, Simple repeats are hittp://encome.wustl.edu/eddy/tRNAscan-SE)). Simple repeats are hittp://encome.wustl.edu/eddy/tRNAscan-SE).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /grammars.complement(join(5439. .5517,5605. .5684,6132. .6212,
complement(join(5439. .5517,5605. .5684,6132. .6212,
6314. .6383,6539. .6613,6693. .6898,7177. .7426,7506. .7551,
8773. .8842,9564. .9633,11257. .11341,11440. .11524,
11608. .11698,12255. .12388))
/codon_start=1
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complement(10in(5540. .5517,5605. .5684,6132. .6212,
6314. .6383,6539. .6613,6693. .6888,7117. .7426,7506. .7551,
8773. .8842,9564. .9633,11257. .11341,11440. .11524,
11608. .11698,12255. .>12557))

complement(5240. .12557)
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SCRTRSSGTLEWTPVKTLALMAKVVVIDDGWSHSVSAFQKWAVLAENLAGSYFVAATS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="GI:13937302"
/translation="MRASVFTGVHSNVPLERVRQLGATLRPGCSSGGARNVGRGSTAA
clone OSJNBb0022E02 is from Oryza sativa chromosome 3 orientation of the sequence is from SP6 to 77 end of the BAC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           http://ftp.genome.washington.edu/RM/RepeatMasker.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /product="hypothetical protein"
/protein_id="AAK50135.1"
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/protein_id="AAK50133.1"
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complement(1271. .1579)
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/qene="OSJNBb0022E02.18"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /chromosome="3"
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24-AUG-2000

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC clade; Panicoideae, Andropogoneae; Zea.

1 (bases 1 to 302)

Harberd, N.P. and Peng, J.

Genetic control of plant growth and development
Patent: WO 9909174-A 16 25-FEB-1999;
HARBERD NICHOLAS PAUL (98); PENG JINRONG (GB)
                                                                                                                                           Triticum aestivum
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae;
Pooldeae; Triticae; Triticum.
1 (bases 1 to 200)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 69 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length 200;
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9
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Pred. No. 0.016;
0; Mismatches
                                                                                                                                                                                                                                                                                                                                   /organism="Triticum aestivum"
/db_xref="taxon:4565"
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172
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188
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58 c 84 g 27 t
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                                         Sequence 69 from Patent WO9909174.
AX005860
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/db_xref="taxon:4577"
                                                                                                AX005860.1 GI:9928855
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Best Local Similarity 93.8%;
Matches 45; Conservative
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                                                                                                                                    bread wheat
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                complement(23124. .23217)
/rpt_family="(GGAGAAn"
complement(join(c23165. .23588, 23765. .23917, 25379. .>25551))
/gene="OSJNBb0022E07."
                                                                                                                                      .25551))
                                                                                                                                                                                                                                      /translation="MAAGSGARAVGDNGGGGPPAPASLPLPPRHPSSPRRTPA
SPIGLLPPRRINCQYSTGSLDESAAGHAVAPTPSPSRRRGADADGESVLGLSSAAAV
WMGAQARSGCEGNASSAAVLSACPYAGDLALAKGENTHGCGVMKGYTHGYTTNSL
VCMYGKLGEMDNAKRAFRDATEKNIVTWNTLITSYATAGLCDEALDVLAQMEQIGGTV
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.

1 (bases 1 to 725)
Harberd, N.P. and Peng, J.
Genetic control of plant growth and development
Patent: WO 9909174-A 19 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
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                                                                           complement(23165...25551)
/gene="OSJNBb0022E02.14"
/note="predicted by fgenesh"
complement(join(23165...23588,23765...23917,25379.
/gene="OSJNBb0022E02.14"
                                                                                                                                                                                                                                                                                                                       Score 45.2; DB 8; Length 122497;
Pred. No. 0.00059;
0; Mismatches 3; Indels 0;
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Pred. No. 0.0056;
0; Mismatches 3;
                                                                                                                                                                                    /product="hypothetical protein"
/protein_id="AAK50123.1"
/db_xref="GI:13937292"
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    .725
    /organism="Oryza sativa"
    /db_xref="taxon:4530"

/rpt_family="AT_rich"
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93.9%;
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94.0%;
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Best Local Similarity 94.0
Matches 47; Conservative
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Matches 46; Conserv
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Gaps

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7 others

24-AUG-2000

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VESMLSELNAPPAPLPPATPAPRLASTSSTVTSGAAAGAGYFDLPPAVDSSSSTYALK
PIPSPVAAPSADPSTDSAREPKRMRTGGSSTSSSSSSSSMDGGRTRSSVVEAAPPAT
QASAAANGPAVPVVVVDTQEAGIRLVHALLACAEAVQQENFSAAEALVKQIPMLASSQ
                                                                                                                                                                                                                                   GGAMRKVAAYFGBALARRYYRPRPPDSSLLDAAFADLLHAHFYESCPYLKFAHFTAN
OALLBAFAGERHYWDFGIRGEMORPALLQALARPGGPPSFRLIGVGPPEDDBTDA
LOQUGWKLAQFAHTTADFEYBYALLABTREGDFDDDBEBEYIANSVFE
LHRLLAQPGALEKVLGTVRAVRPRIVTVVEQEANHNSGTFLDRFTESLHYYSTMFDSL
                                                                                                                                                                                                                                                                                                      EGAGAGSGQSTDASPAAAGGTDQVMSEVYLGRQICNVVACEGAERTERHETLGQWRSR
LGGSGFAPVHLGSNAYKQASTLLALFAGGDGYRVEEKDGCLTLGWHTRPLIATSAWRV
                                                                                                                                                 /translation="mKREYQDaGGSGCDMGSSKDKMMAAAAGAGEGEEEDVDELLAAL
GYKVRSSDMADVAQKLEQLEMAMGMGGVGGAGATADDGFVSHLATDTVHYNPSDLSSW
                                                                                        /product="gibberellin response modulator"
/protein_id="CAB51557.1"
/db_xref="G1:5640155"
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                                                               /note="GAI ortholog"
                                                                               /codon_start=
                                                                                                                                                                                                                                                                                                                                                                                                                            78.0%;
86.3%;
              /gene="d8"
1. .>1890
                                              /gene="d8"
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Best Local Similarity
Matches 44; Conserv
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Spermatophyta; Magnoliophyta; Lillopsida; Poales; Poaceae; PACC
clade; Panicoideae; Andropogoneae; Zea.
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Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; PACC
clade; Panicoldeae; Andropogoneae; Zea.
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Peng,J., Richards,D.E., Hartley,N.M., Murphy,G.P., Devos,K.M., Filntham,J.E., Beales,J., Fish,L.J., Worland,A.J., Pelica,F., Sudhakar,D., Christou,P., Snape,J.W., Gale,M.D. and Harberd,N.P., Green revolution' genes encode mutant gibberellin response
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Submitted (25-MX-1999) Richards D.E., Molecular Genetics, John Innes Centre, Colney Lane, NR4 7UJ, UNITED KINGDOM
Location/Qualifiers
1. .1890
/organism="Zea mays"
/db_xref="taxon:4577"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Zea mays partial d8 gene for gibberellin response modulator. AJ242530 AJ242530.1 GI:5640154
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                                                                              Length 302;
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0.12;
            Score 39.8; DB Pred. No. 0.13; 0; Mismatches
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Pred. No. 0.12;
0; Mismatches
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Sequence 17 from Patent W09909174.
AX005808
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/db_xref="taxon:4577"
121 c 139 q
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Harberd, N.P. and Peng, J.
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1 Similarity 86.3%;
44; Conservative
            78.0%;
86.3%;
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            Query Match 78.0
Best Local Similarity 86.3
Matches 44; Conservative
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Best Local Similarity
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0; Mismatches

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Length 1890;

Score 39.8; DB 8; Pred. No. 0.071;

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Patent: WO 9909174-A 15 25-FEB-1999;
HARBERD NICHOLAS PAUL (GB); PENG JINRONG (GB)
Location/Qualitiers
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New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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Copyright (c) 1993 - 2000
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Listing first 45 summaries
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Result Š a

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant: This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable to breatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants mutant plants which are essistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence is derived from the wheat rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   100.0%; Score 51; DB 20; 100.0%; Pred. No. 5.6e-08;
                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 51 BP; 7 A; 16 C; 21 G; 7 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   0; Mismatches
  Claim 3; Page 53; 88pp; English.
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Best Local Similarity 100.
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Gaps

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Length 51; Indels

AAX36263 standard; DNA; 453 BP

RESULT

AAX36263;

16-JUL-1999 (first entry)

Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; DNA sequence obtained after sequencing wheat Rht clone 14al. paclobutrazol; ss.

Triticum aestivum

WO9909174-A1

25-FEB-1999

98WO-GB02383 07-AUG-1998; 97GB-0017192. 13-AUG-1997;

(PLAN-) PLANT BIOSCIENCE LTD.

Richards Harberd NP, Peng J,

DE;

WPI; 1999-181040/15

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

Disclosure; Fig 2b(9); 88pp; English.

The specification describes polypeptides encoded by the Rht gene (and 1ts homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants

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may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 14al.
                                                                                                                                             Gaps
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is
                                                                                                                                                                                                                                                                                                                                              Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; ss.
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                                                                                                                                                                   Length 453;
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                                                                                   Sequence 453 BP; 85 A; 136 C; 158 G; 67 T; 7 other;
                                                                                                                   100.0%; Score 51; DB 20;
100.0%; Pred. No. 6.2e-08;
ive 0; Mismatches 0;
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                                                                                                                                 Best Local Similarity 100.
Matches 51; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-181040/15
                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAY02540.
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                                                                                                                       Query Match
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Sequence 2125 BP; 325 A; 768 C; 723 G; 309 T; 0 other;

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by the plant. This growth inhibition is antagonised by plaberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps
                                     Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            dwarf but let crop plants grow tall. The present sequence represents the composite DNA sequence of wheat Rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                        Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
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Length 2125;
                                                                                    0; Indels
                                                                   1 gacgagctgctggcggcgctcgggtacaaggtgcgcgcctccgacatggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 2709 BP; 473 A; 900 C; 823 G; 482 T; 31 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               100.0%; Score 51; DB 20; 100.0%; Pred. No. 6.6e-08;
100.0%; Score 51; DB 20;
100.0%; Pred. No. 6.5e-08;
ive 0; Mismatches 0;
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                                                                                                                                                                                                                                                                                        Composite DNA sequence of wheat Rht gene.
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                                                                                                                                                                                    AAX36275 standard; DNA; 2709
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Matches 51; Conservative
               Local Similarity 100.
es 51; Conservative
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                                                                                                                                                                                                                                                                                                                                                         paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                           Triticum aestivum.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in
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                                                                                                                                                 gene; homologue; Triticum aestivum; wheat; growth inhibition; agonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
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                                                                                                                DNA sequence obtained after sequencing wheat Rht clone 5al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 gacgagctgctggcggcgctcgggtacaaggtgcgcgcctccgacatggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   162 GNCGNGCTGCTGGCGCGCTCGGGTACAAGGTGCGCGCCTCCGACATGGCG
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Rice EST D39460 sequence, homologous to wheat Rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 324 BP; 39 A; 141 C; 85 G; 56 T; 3 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Score 49; DB 20; L
Pred. No. 2.7e-07;
0; Mismatches 2;
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                  BP.
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96.1%;
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AAX36273/c
ID AAX36273 standard; DNA; 324
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                                                                                  (first entry)
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Best Local Similarity 96.19
Matches 49; Conservative
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                                                                                                                                                                                                                                                                                                                                                                                                                                               WPI; 1999-181040/15
                                                                                                                                                                                  paclobutrazol; ss.
                                                                                                                                                                                                                Friticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                (PLAN-) PLANT
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                                                                                                                                                                    antagonist;
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                                                 AAX36273;
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AAX36277
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by gluberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gluberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gluberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial cDNA sequence of rice AAD39460 (a wheat Rht gene homologue).
                                                                                                                                                                                                                                                                                                               New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 725 BP; 98 A; 226 C; 276 G; 119 T; 6 other;
                                                                                                                                                                                                               Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                      Disclosure; Fig 4a; 88pp; English.
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                                                       07-AUG-1998;
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       25-FEB-1999
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Matches
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST; ss.
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Best Local Similarity 94.0 Matches 47; Conservative
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                                                                                                          Oryza sativa
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Gaps

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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                           DNA sequence obtained after sequencing wheat Rht clone 14al.
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AAX36276

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WPI; 1999-181040/15

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Trilicum Aestivum, inhibit growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence was cobtained after partially sequencing wheat Rht clone 14al.
New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                  Disclosure; Fig 2b(12); 88pp; English
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Sequence 200 BP; 24 A; 58 C; 84 G; 27 T; 7 other;

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Gaps
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 Score 43.2; DB 20; Length 200;
Pred. No. 1.9e-05;
0; Mismatches 3; Indels 0
                                              Query Match 84.7%;
Best Local Similarity 93.8%;
Matches 45; Conservative
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AAX36281 standard; DNA; 302 AAX36281; δ AX36281 ESULT

Partial sequence of the maize D8-1 allele. 16-JUL-1999 (first entry)

gene; homologue; Triticum aestivum; wheat; growth inhibition; agonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize; ss antagonist;

Zea mays.

WO9909174-A1

25-FEB-1999

98WO-GB02383. 07-AUG-1998;

97GB-0017192 13-AUG-1997;

DE; Richards (PLAN-) PLANT BIOSCIENCE LTD Harberd NP, Peng J,

WPI; 1999-181040/15. P-PSDB; AAY02542.

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

Disclosure; Fig 11a; 88pp; English.

The specification describes polypeptides encoded by the Rht gene (and

its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globerallin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with globerallin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberallin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberallin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberallin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the maize D8-1 allele.

Sequence 302 BP; 52 A; 82 C; 123 G; 45 T; 0 other;

ö Gaps ó Length 302; Indels Score 39.8; DB 20; Pred. No. 0.00024;); Mismatches 7; 0; Mismatches Query Match 78.0%; Best Local Similarity 86.3%; Matches 44; Conservative

51 1 gacgagctgctggcggcgctcggggtacaaggtgcgcgcctccgacatggcg g δ

10 AAX36282 RESULT

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BP AAX36282 standard; DNA; 371

AAX36282;

(first entry) 16-JUL-1999 Partial sequence of the maize D8-2023 allele.

Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize; ss.

Zea mays.

WO9909174-A1 A PART A

25-FEB-1999

98WO-GB02383. 07-AUG-1998; 97GB-0017192. 13-AUG-1997; (PLAN-) PLANT BIOSCIENCE LTD

Richards DE; Harberd NP, Peng J,

WPI; 1999-181040/15. P-PSDB; AAY02543.

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype New Triticum Aestivum polynucleotides provides inhibition of the growth of pl

Disclosure; Fig 11c; 88pp; English.

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to

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Gaps

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Indels

Pred. No. 0.00026;

86.38;

44; Conservative

Best Local Similarity Matches 44; Conserv

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0; Mismatches

308 gatgagetgetggeegegetegggtacaaggtgegttegteggatatggeg 358

BP

AAX36283 standard; DNA; 416

AAX36283

RESULT

gacgagetgetggcggcgctcgggtacaaggtgcgcgcctccgacatggcg

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibitton is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring adwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin blosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents
                                                                                                              Local Similarity 86.3
hes 44; Conservative
                                                                                                                                                                                                                                                                                                                                                                   paclobutrazol; maize; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-181040/15.
P-PSDB; AAY02541.
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                                                                                                                                                                                                                                                                                                                                                      antagonist;
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                                                                                                   Query Match
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8888838
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compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the maize D8-2023 allele.
                                                                                                                                                                                                                                                                                                                                           Gaps
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                                                                                                                                                                                                                                                                                                                                       ö
                                                                                                                                                                                                                                                                          Length 371;
                                                                                                                                                                                                                                                                                                                                                                                                                                             Indels
                                                                                                                                                                                                                                                                                                                                                                                                       1 gacgagetgetggeggegetegggtaeaaggtgegegeeteegaeatggeg
                                                                                                                                                                        Sequence 371 BP; 56 A; 121 C; 139 G; 55 T; 0 other;
                                                                                                                                                                                                                                                                    78.0%; Score 39.8; DB 20;
86.3%; Pred. No. 0.00025;
iive 0; Mismatches 7;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Disclosure; Fig 9a; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Maize lal genomic clone sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AAX36280 standard; DNA; 2255 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANT BIOSCIENCE LTD
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>mologue; Triticum aestivum; wheat; growth inhibition; gibberellin; dwarf phenotype; gibberellin biosynthesis;

Partial sequence of the wheat rht-10 allele.

Rht gene; homologue;

antagonist;

paclobutrazol; ss. Triticum aestivum.

(first entry)

16-JUL-1999

AAX36283;

The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globerallin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the treatment with globerallin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with uld-type, the dwarfing being globerallin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit globerallin blosynthesis, such as paclobutrazol, e.g. to allow use of a globerallin blosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the wheat rht-10 allele. Gaps ö Length 416; Indels Sequence 416 BP; 59 A; 168 C; 129 G; 60 T; 0 other; 76.5%; Score 39; DB 20; 1 100.0%; Pred. No. 0.00045; tive 0; Mismatches 0; Conservative Local Similarity nes 39; Conserv Query Match Best Loca Matches 셤 ó

New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype

Richards

Peng J,

Harberd NP,

WPI; 1999-181040/15.

P-PSDB; AAY02544

(PLAN-) PLANT BIOSCIENCE LTD.

98WO-GB02383.

37-AUG-1998; 13-AUG-1997;

25-FEB-1999

97GB-0017192

Oisclosure; Fig 12a; 88pp; English.

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RESULT

Length 2255;

DB 20;

Score 39.8;

78.08;

Query Match

Sequence 2255 BP; 334 A; 817 C; 737 G; 367 T; 0 other;

the maize lal genomic clone sequence.

AAZ60717;

AAZ60717

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A library of S. clavuligerus NRRL 5741 genomic DNA fragments (15-22 kb) constructed in cosmid pLAFR3 was screened for the cla gene using a probe based on a partial N-terminal sequence from the CLA enzyme. Isolated clone K6L1 included a 15kb fragment having the sequence given in AAQ91580 that included the cla gene (ORF4).
                                                                                              Clavulinic acid; clavulinate; antibiotic; beta-lactamase-inhibitor;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 1995-207301/28.
P-PSDB; AAR77858; AAR77859; AAR77860; AAR77861; AAR77862; AAR77863;
AAR77864; AAR77865; AAR77866; AAR77867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clavulanic acid biosynthesis enzymes and corresp. DNA - useful for biosynthesis of the antibiotic in Streptomyces hosts which do not
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              complement (10998..12296)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             complement (12662..13365)
                                                                                                                                                                                              complement (49..1745)
                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Paradkar AS;
                                                                                                                                                                                                                                                                                                                                                                            /label= ORF4
/note= "cla gene"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Disclosure; Fig.2; 41pp; English.
                                                                S. clavuligerus cla gene region.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= j
/label= ORF10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        naturally produce clavulanate
                                                                                                                                                                                                                                                           /*tag= b
/label= ORF2
3940..5481
                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= e
/label= ORF5
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label= ORF1
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5654..6595
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/label= ORF8
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/label= ORF7
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                                                                                                                                                                                                                                                                                                                                                                                                                                                          7895..9076
                                                                                                                                                                                                                                                 2216..3937
                                   (first entry)
                                                                                                                                                 Streptomyces clavuligerus.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-OCT-1993;
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                                 13-NOV-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CA2108113-A.
                                                                                                                 cla gene;
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AAQ91580;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Preparation of N-substituted azetidinone, useful as intermediate for clavulanic acid, by cyclisation of N-substituted aminopropanoic acid in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes an beta-lactam synthetase polypeptide. The enzyme is encoded by orf3 of the clavulanic acid biosynthesis cluster. This enzyme converts a beta-anino acid (formed from arginine and pyruvate) into the beta-lactam form, early in the clavulanic acid biosynthesis pathway. The beta-lactam synthetase enzyme is used for 2-aminopropanoic acid derivatives. The method is particularly used to make (25)-5-quanidino-2-(2-oxo-azetidin-1-yl)pentanoic acid from N2-(2-carboxyethyl)-(5)-arginine. (25)-5-quanidino-2-(2-oxo-azetidin-1-yl)pentanoic acid is an intermediate for clavulanic acid, a known inhibitor of beta-lactamase, used in combination with beta-lactam antibiotics for treatment of infections. More generally, N-substituted azetidinones are intermediates for other clavulams and
                                                                                                                                            Beta-lactam synthetase; orf3; clavulanic acid biosynthesis cluster; beta-amino acid; beta-lactam; clavulanic acid biosynthesis; N-substituted azetidinone; clavulanic acid; beta-lactamase inhibitor; (2S)-5-guanidino-2-(2-ox-azetidin-1-yl)pent hanoic acid; beta-lactam antibiotic; infection; clavulam; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 1542 BP; 190 A; 591 C; 557 G; 204 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Score 29.8; DB 21;
Pred. No. 0.43;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12;
                                                                                                             DNA encoding a beta-lactam synthetase enzyme.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      0.43;
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                                                                                                                                                                                                                                                                            Location/Qualifiers
4..1542
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            presence of beta-lactam synthetase
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                AAZ60717 standard; DNA; 1542 BP
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75.5%;
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                                                                               16-MAY-2000 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Barton B, McNaughton HJ,
                                                                                                                                                                                                                                               Streptomyces clavuligerus.
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P-PSDB; AAY68875.
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Best Local Similarity
Matches 37; Conserv
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Sequence 15079 BP; 2097 A; 5488 C; 5324 G; 2170 T; 0 other;

AAQ91580 standard; DNA; 15079 BP

AAQ91580 ID AAQ9 XX

RESULT

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the conferring a dwarf phenotype on a plant which is correctable used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerellin-insensitive. Taller plants wild-type, the dwarfing being globerellin-insensitive. Taller plants the plant of interest. Plants may be made which are resistant to compounds which inhibit globerellin blosynthesis, such as paclobutrazol, e.g. to allow use of a globerellin blosynthesis, such as paclobutrazol, e.g. to allow use of a globerellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was obtained after partially sequencing wheat Rht clone 14al.
                                    ö
                                        Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                    Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
Length 15079;
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                                                                                                                                                                                                                                                                                                                 DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                            51
                                      Indels
                                                                         3 cgagctgctggcggcgctcggggtacaaggtgcgcgcctccgacatggcg
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                                    12;
   DB 16;
Query Match 58.4%; Score 29.8; DB Best Local Similarity 75.5%; Pred. No. 0.47; Matches 37; Conservative 0; Mismatches
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                                                                                                                                                                                                       AAX36261 standard; DNA; 309 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             WPI; 1999-181040/15.
                                                                                                                                                                                                                                                                                                                                                                                         paclobutrazol; ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            07-AUG-1998;
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Gaps

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57.6%; Score 29.4; DB 20; Length 309; Ilarity 93.8%; Pred. No. 0.55; Conservative 0; Mismatches 2; Indels 0

Query Match Best Local Similarity Matches 30; Conserv

tegggtacaaggtgegeeteegacatggeg 51

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Search completed: December 19, 2001, 22:25:14 Job time: 5581 sec

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Eukaryota; Varidiplantae; Streptophyta; Embryophyta; Tracheophyta; Bukaryota; Varidiplantae; Streptophyta; Enhartoldeae; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Spermatoldeae; Oryzeae; Oryzea; Li (bases 1 to 263)
E (bases 1 to 263)
E Sasaki,T., Miyao,A. and Yamamoto,K.
Rice cDNA from callus 1995
L Unpublished (1995)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7448
                                   NF117E10S
NF099H09S
EST530226
NF072A05S
NF072A07S
NF107A12S
                 MtBA31D06
MtBA44B05
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EST508687
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NF010B04S
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M54G7STM
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605040E01
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sf95f03.y
AV643605
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AL233043 T
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                 AL369482 A
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B1308816 A
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AW584561 A
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Oryza sativa cDNA, mRNA sequence.
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/db_xref="taxon:4530"
/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
64 c 116 g 35 t 2 others
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/organism="Oryza sativa"
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Copyright (c) 1993 - 2000 Compugen Ltd.
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Best Local Similarity 94.0%;
Matches 47; Conservative
                                                                                                  305-8602, Japan
Tel: 81-298-38-7441
Fax: 81-298-38-7468
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Gukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta: Spermatophyta: Magnoliophyta: Liliopsida: Poales: Poaceae;
Ehrhartoideae: Oryzeae: Oryza.

1 (bases 1 to 388)

2 (contect: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki

3 (contect: Takuji Sasaki

4 (contect: Takuji Sasaki

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Fax: 81-298-38-7468
Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/.
Location/Qualifiers
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Oryza sativa.

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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae; Ehrbartoideae; Oryzeae; Oryza.

Ehrbartoideae; Oryzeae; Oryza.

Ehrbartoideae; Oryza.

Ehrbartoideae; Oryza.

Ehrbartoideae; Oryza.

Enter 1 (bases 1 to 467)

Rice cDNA from etiolated shoot (2001)

Contact: Takuji Sasaki

National Institute of Agrobiological Resources

Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan

Tel: 81-298-38-7441

Fax: 81-298-38-7468

Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /db_xref="texponents | 20" | /db_xref="texponents | 20" | /db_xref="texponents | 20" | /clone="E60220" | /clone="texponents | 20"                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
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Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
                                                                                                                                                                                                                                                      Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT ='RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps
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6
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length 399;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone="S0583"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Indels
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/note="Etiolated shoot (8 days old)"
136 c 176 9 65 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Query Match 88.6%; Score 45.2; DB 10; Best Local Similarity 94.0%; Pred. No. 0.00073; Matches 47; Conservative 0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 45.2; DB 10;
Pred. No. 0.00073;
0; Mismatches 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     1. .399 /organism="Oryza sativa"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /strain="Nipponbare"
                                                                                                                                                                                                                                                                                                                                                                                                            Location/Qualifiers
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REFERENCE AUTHORS

ORGANISM

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ACCESSI VERSION

KEYWOR SOURCE

BF26801 LOCUS

RESULT

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JOURNAL COMMENT

TITE

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/urganism="Glycine max"
/cultivar="Harosoy 63"
/cultivar="Harosoy 63"
/dultivar="Harosoy 63"
/do.xef="texaon:3847"
/clone_lib="GmaxSC"
/tissue_type="Seed coats"
/tlab_bost="E. coli strain XLOLR"
/lab_bost="E. coli strain XLOLR"
/note="Vector: pBk-CNM's Site_1: EcoRI; Site_2: XhoI; This
seed coats in mid per seed. Traces of pod and
embryo tissue also present. Complementary DNA was
synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adopters were ligated to the
blunt-ended cDNA fragments and the products were digested
with XhoI for directional cloning into lambda ZAP Express
vector: This lambda library was amplified once using E.
coli host strain XII Blue MRF'. Inserts were then
subcloned by mass excision using ExAssist helper phage for
conversion into phagemid vector pBK-CMV in E. coli host
strain XLOLR."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
  Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length 711;
                                                                                                                                                                                                    1391 Sandford Street, London, Ontario, Canada N5V 4T3
Tel: 519 457 1470
Fax: 519 457 3997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        174 GACGAGTTGCTGGCGGCGTACAAGGTTCGTGCTTCCGACATGGC 223
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1391 Sandford Street, London, Ontario, Canada N5V
Tel: 519 457 1470
Fax: 519 457 3997
Email: glizenm@em.agr.ca.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Indels
                                                                                        Haris, N., Chapman, B. P. and Gijzen, M.
Gene expression in developing soybean seed coats
Unpublished (2000)
Contact: Gijzen M
Agriculture and Agri-Food Canada
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Harris, N., Chapman, B.P. and Gijzen, M. Gene expression in developing soybean seed coats Unpublished (2000)
Contact: Gijzen M
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 EST
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                                                                                                                                                                                                                                                                                                  Location/Qualifiers
1. .711
                                                                                                                                                                                                                                                                                      Email: gijzenm@em.agr.ca
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207 c
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                                                                    (bases 1 to 711)
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                                                   Glycine.
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                                                                                                                      TITLE
JOURNAL
COMMENT
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COMMENT
                                                                       REFERENCE
AUTHORS
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SOURCE
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BE659954
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                                                                                                  BF268018 844 bp mRNA EST 09-MAR-2001
HV_CEG0019J17f Hordeum vulgare seedling green leaf EST library
HVCDNA0004 (Erysiphe infected & control) Hordeum vulgare cDNA clone
BF268018
                                                                                                                                                                                                                                                                                                                                                        Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Sperimatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooideae; Triticeae; Hordeum.
; Triticeae; Hordeum.
(Apases 1 to 844)
                                                                                                                                                                                                                                                                                                                                                                                                                                                 Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo, T., Saski, C., Schwartzbeck, J., Simmons, J., Choi, D.W., Main, D. and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ö
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xho1; For
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/Darley/ To sorder a clone see http://www.genome.clemson.edu/orders" 290 c 276 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glycine max
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Development of a genetically and physically anchored EST resource for barley genomics (for barley genomics (2000) on Nov 17, 2000 this sequence version replaced gi:11199013. Contact: Wing RA Clemson University Genomics Institute clemson University
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Gaps
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /clone_"HV_CEMONIGJI7f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HVCDMA0004 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="fJC121"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ö
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Pred. No. 0.0011;
0; Mismatches 4; Indels 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  60 GACGAGCTGCTGGCCGCGCTCGGCTACAAGGTGCGGGCGTCCGACATGCG 310
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          21
1077 GmaxSC Glycine max cDNA, mRNA sequence. BE659955
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism-"Hordeum vulgare"
/cultivar-"CI16155 (Mla13)"
/db_xref-"taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: rwing@clemson.edu
Seq primer: AATAAACCCTAAAGGG
High quality sequence stop: 587.
Location/Qualiflers
                                                                                                                                                                                                                                                               BF268018.2 GI:13263734
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               BE659955.1 GI:9985949
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92.2%;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1. .844
                                                                                                                                                                                                                                                                                                            barley.
Hordeum vulgare
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             soybean.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Wood, T.
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source
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SOURCE
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06-SEP-2000

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Query Best BE6599\$5

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Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                       Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1. 484
/Organism=Lotus japonicus"
/Organism=Lotus japonicus"
/Ob_xref="taxon:33.05"
/clone="MWM005b04_r"
/clone="MWM005b04_r"
/clone="Lib="Lotus japonicus young plants (two-week old)"
/dev_stage="Young plants (two-week old)"
/note="Vector: pBluescriptii SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
                                                                                                                                                                                                                AV422153 484 bp mRNA EST 23-MAY-2000 AV422153 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM005b04_r 5', mRNA sequence.
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Generation of 7137 non-redundant expressed sequence tags from
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                                            9; Indels
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The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
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0; Mismatches
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DNA Res. 7 (2), 127-130 (2000)
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AV422153.1 GI:7776718
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82.0%;
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  41; Conservative
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Best Local Similarity
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TITLE
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TITLE
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KEYWORDS
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KEYWORDS
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                                                             /clone_lib_amaxSc_
/tissue_type="Seed coats"
/lab_host="E. coil strain XLOLR"
/note="Vector: pBk-CMM'; Site_i: ECORI; Site_2: XhoI; This
/note="Vector: primer seed coats in mid to late developemental stage
/notesized from mRNA using an XhoI-poly(dT)
/note="Vector: primer: ECORI adopters were ligated to the
blunt-ended cDNA fragments and the products were digested
with XhoI for alrectional cloning into lambda ZAP Express
vector: This lambda library was amplified once using E.
coli host strain XLOLR: Inserts were then
subcloned by mass excision using Exassist helper phage for
conversion into phagemid vector pBk-CM in E. coli host
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Contact: Yasukazu Nakamura
The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/
Location/Qualifiers
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//clone_llb="Lotus japonicus young plants (two-week old)"
//dev_stage="young plants (two-week old)"
//dev_stage="young plants (two-week old)"
//note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
XhOI; isolate=MIyakojima MG-20"
// 0 c 101 g 90 t
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Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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Pred. No. 0.26;
0; Mismatches 6;
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/db_xref="taxon:34305"
  /organism="Glycine max
                      /cultivar="Harosoy 63'/db_xref="taxon:3847"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 113 g
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AV410222.1 GI:7723076
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Best Local Similarity 87.0%;
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Best Local Similarity
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ACCESSION VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL MEDLINE COMMENT

LOCUS

RESULT AV410222

BASE COUNT ORIGIN

Matches

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Gaps

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source

FEATURES

BASE COUNT ORIGIN

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51

week-old Lotus

FEATURES

Query

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ACCESSI KEYWORI

MEDIT

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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                 Lotus japonicus
Sukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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//note="Organ: Nodule; Vector: psPORT1; Site_1: SalI;
Site_2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
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                                                                                                                                                                                                                                                                                                                                                                                                                                                    (bases 1 to 586)
Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
Contact: Udvardi MK
                                                                                                                                                                                         BI419686 586 bp mRNA EST 15-AUG-2001
LjNEST47e12r Lotus japonicus nodule library 5 and 7 week-old
japonicus cDNA 5', mRNA sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Max Planck Institute of Molecular Plant Physiology Am Muchlenberg 1, 14476 Golm, Germany Fax: 49 331 567 8250 Email: udvardi@mpimp-golm.mpg.de
                                                                                 172 GACGAGCTTCTCGCGGTGGTGGGTTACAAGGTGAGGTCATCAGACATGGCG
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                                           1 gacgagetgetggggggggegetecgggtgcgcgcctccgacatggcg
11; Indels
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Mismatches
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High quality sequence stop: 586.
Locatton/Qualifiers
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BE321891.2 GI:11964088
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BI419686.1 GI:15190709
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173 c
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Matches 40; Conserv
40;
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COMMENT
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AUTHORS
  Matches
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                                 The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: yanakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                  /organism="Lotus japonicus"
/db_xef="teaxon:34305"
/clone="MMLOGleil_r"
/clone_lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Vector: pBluescriptil SR-; Site_l: EcoRI; Site_2:
XhoI: _isolate=Miyakojima_MG-20"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 478)
Colebatch, G., Freund, S., Trevaskis, B. and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
Contact: Udvardi MK
                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone_lib="Lotus japonicus nodule library 5 and 7 week-old"
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                                                                                                                                                                                                                                                                                                                                                                                                              Length 365;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             18 GACGAGCTTCTCGCGGTGGTGGGTTACAAGGTGAGGTCATCAGACATGGCG 168
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Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
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                                                                                                                                                                                                                                                                                                                                                                                                              DB 10;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         11;
                                                                                                                                                                                                                                                                                                                                                                                                              Score 33.4; DB
Pred. No. 1.9;
0; Mismatches
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/organism="Lotus japonicus"
/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
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Pred. No. 2;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: udvardi@mpimp-golm.mpg.de
Seg primer: T7
High quality sequence stop: 478.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                        102 g
                      Contact: Yasukazu Nakamura
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78.4%;
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illarity 78.4%;
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Lotus japonicus
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es 40; Conserv
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Gaps

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Indels

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FEATURES

Query Best L

Length 586;

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Query Match 63.5
Best Local Similarity 78.0
Matches 39, Conservative
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                            Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.X., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /dev_arge="mature"
//dev_arge="mature"
//dev_arge="mature"
//note="Vector: Lambda Zap; Library was produced from fully
sepanded M. truncatula leaves of plants fed upon by
Spodoptera exigua (beet armyworm) for 24 hours. Systemic
(undamaged leaves from injured plants) and wounded leaves
were harvested and pooled."
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Bukaryota, Vitidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Emall: seqreféquencope.cns.fr, whe : www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
Mr.estétoulouse.inra.fr Website: .
http://sequence.toulouse.inra.fr/Mtruncatula.html).
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                                                                                                                                                           Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:9195668
Contact: Korth K
Dept. of Plant Pathology
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/db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="inseqt herbivory"
/tissue_type="local and systemic leaves"
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78.0%; Pred. No. 3.8;
:ive 0; Mismatches
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   (bases 1 to 372)
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Best Local Similarity
Matches 39; Conserv
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papliionoideae; Trifolleae;
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Bp 191 91006 EVRX cedex - France
Email: seqref@genoscope.cns.fr. Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Woleculaire des Relations Plantes Microorganismes,
CNRS.INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
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Journet, E. P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Journet, E. P., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
, V. and Gamas, P.
Medicago truncatula ESTs from nitrogen-starved roots
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/dev_stage="harvested after 3 days of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoR1; Site_2:
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                                          organism="Medicago truncatula"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Score 32.4; DI
Pred. No. 3.8;
0; Mismatches
                                                         /cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtBA30E09"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /cultivar-"Jemalong"
/db_xref-"taxon:3880"
/clone-"MtBA31D06"
Location/Qualifiers
                                                                                                                            /clone_lib-"MtBA"
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XhoI; Plants were grown in an aeroponic chamber for 14 days on nitrogen-rich medium followed by 3 days on N-free medium. RNA was extracted from root tips (1-3 cm). cDNA was prepared from polyA+ enriched RNA. The cDNA was directionally ligated into Uni-zapXR vector from Stratagene and packaged using Giapack Gold packaging extracts. Plasmids containing cDNA inserts were mass-excised from phage stocks using ExAssit helper phage and propagated in SOLR cells. Clone ordering and sequencing was performed by the Centre National de Sequencage (Genoscope, EVTY, France)."
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172 BASE COUNT ORIGIN

Gaps ö Query Match 63.5%; Score 32.4; DB 10; Length 458; Best Local Similarity 78.0%; Pred. No. 3.8; Matches 39; Conservative 0; Mismatches 11; Indels 0

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Search completed: December 19, 2001, 21:14:15 Job time: 15337 sec

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                                                          Query Match
   ; Search time 69.5 Seconds
(without alignments)
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Sequence 13, Appl
Sequence 1, Appli
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Sequence 39, Appl
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Sequence 5,
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Sequence 1,
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/cgn2_6/ptodata/2/ina/5B_COMB.seq:*
/cgn2_6/ptodata/2/ina/6A_COMB.seq:*
/cgn2_6/ptodata/2/ina/6B_COMB.seq:*
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:*
/cgn2_6/ptodata/2/ina/pcTUS_COMB.seq:*
                          GenCore version 4.5
Copyright (c) 1993 - 2000 Compugen Ltd.
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PCT-US91-00399-1

US-08-440-856A-1

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US-09-103-840A-1
US-08-998-416-401
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                                                                                                                                                                                                             December 19, 2001, 18:34:13
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Listing first 45 summaries
                                                                                                                                                     using sw mode]
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                                                                                                                                                                                                                                                                                                                        US-09-485-529-105
51
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                                                                                                                                                                                                                                                                                                                                        Title:
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Sequence 23, Appl
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appli
Sequence 1, Appl
Patent No. 5229279
Patent No. 5512669
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Sequence 3, 14
Sequence 1, 14
Sequence 2, 14
Sequence 1, 16
Sequence 2, 17
Sequence 2, 18
Sequence 2, 18
Sequence 2, 18
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Susan E. Jensen
APPLICANT: Susan B. Jensen
APPLICANT: Kwamena A Aidoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavu.
Patent No. 6232166
TITLE OF INVENTION: Acid Biosynthesis
NUMBER OF SEQUENCES: 25
CORRESPONDENCE ADDRESS:
ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
CITY: Washington
STATE: D.C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
ZIP: ZBOADALE FORM:
COMPUTER READBLE FORM:
COMPUTER: IBM PC COMPATIBLE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30 (EPO)
                  US-08-241-943-23
US-08-254-357-1
US-09-061-702-3
US-09-046-992-1
US-08-510-646B-17
5229279-5
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US-08-743-637B-20
US-08-526-840B-20
US-08-748-170A-3
US-09-047-148-1
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CLASSIFICATION NUMBER: US 08/790,462
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-3AN11997
ATTORNEY/AGENT INFORMATION:
NAME: D. DOUGLAS FLICE
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/F57452US2
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202 39305350
TELEPHONE: (202) 39305350
TELEPA: (CA2) 39305350
TELERIS RCA 246893 IDEA UR
INFORMATION FOR SEQ ID NO: 16:
US-09-103-840A-1
                                                                                                                                                                                                                                                              US-08-006-676B-2
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                                                                                                                                                                                                                                                                                                                                                                                                                     ALIGNMENTS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Sequence 16, Application US/09385028
Patent No. 6232106
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ; MOLECULE TYPE: DNA (genomic) US-09-385-028-16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  LENGTH: 1542 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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Length 1542;

4;

DB

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APPLICANT: Peng, Jinrong
APPLICANT: Carol, Pierre
APPLICANT: Richards, Donald E
TITLE OF INVENTION: Nucleic acid encoding GAI gene of Arabidopsis thaliana
FILE REFERENCE: 620-45
                        DNA Sequence Encoding Enzymes of Clavulanic
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 cgagetgetgetgggggegeteggggtacaaggtgegegeeteegaeatggeg 51
                                                                                                                                   ADDRESSEE: JACOBSON, PRICE, HOLMAN & STERN, PPLC
STREET: The Jenifer Buliding, 400 Seventh Street, N.W.
                                                                                                                                                                                                                                                                                                                                                    SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/385,028
                                                                                                                                                                                                                                                                                                                                                                                                                                          CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452USZ
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Score 29.8; DB
Pred. No. 0.24;
0; Mismatches
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CURRENT FILING DATE: 1998-08-12
EARLIER APPLICATION NUMBER: PCT/GB97/00390
EARLIER FILING DATE: 1997-02-12
EARLIER FILING DATE: 1997-02-12
EARLIER FILING DATE: 1997-02-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Streptomyces clavuligerus US-09-385-028-1
                                                                    Acid Biosynthesis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 1, Application US/09117853
Patent No. 6307126
                                                                                                                                                                                                                                                                                         MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
      Ashish S. Paradkar
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                GENERAL INFORMATION:
APPLICANT: Harberd, Nicholas P
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEPHONE: (202 638-6666
TELEFAX: (202) 39305350
TELEX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 1:
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75.5%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   LENGTH: 15079 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Query Match
Best Local Similarity 75.5
Matches 37; Conservative
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                                                                                        NUMBER OF SEQUENCES: 2:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQ ID NOS: 12
                                               Patent No. 6232106
TITLE OF INVENTION:
                                                                                                                                                                                                                                                                                                                                    OPERATING SYSTEM:
                           TITLE OF INVENTION:
                                                                                                                                                                                 Washington
                                                                                                                                                                                                                            U.S.A.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                 CITY: Wash:
STATE: D.C
                                                                                                                                                                                                                                                20004
      APPLICANT:
                                                                                                                                                                                                                         COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   RESULT 4
JS-09-117-853-1
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                             Gaps
                                                                                                                                                                                                                                                                                       APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aldoo
APPLICANT: Ashish S. Paradkar
TITLE OF INVENTION: DNA Sequence Encoding Enzymes of Clavulanic
Patent No. 6232106
TITLE OF INVENTION: Acid Biosynthesis
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                                                                                             909 CGAGCTGCTGCTGCTGCTGCTGCGGTGTGGGCCTCCGAGTCGGTG 957
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 cgagctgctgcggcgctcgggtacaaggtgcgcgcctccgacatggcg 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STREET: The Jenifer Buliding, 400 Seventh Street, N.W CITY: Washington
                           12; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/385,028
                                                                      cgagctgctggcggcgctcgggtacaaggtgcgcgcctccgacatggcg
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/790,462
FILING DATE: 29-JAN-1997
ATTORNEY/AGENT INFORMATION:
NAME: D. Douglas Price
REGISTRATION NUMBER: 24,514
REGISTRATION NUMBER: 24,514
REFERENCE/DOCKET NUMBER: 1418/P57452US2
TELECOMMUNICATION INFORMATION:
TELEPAX: (202 383-666
TELEPAX: (202) 39305350
TELETX: RCA 248593 IDEA UR
INFORMATION FOR SEQ ID NO: 13:
      Pred. No. 0.23;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         58.4%; Score 29.8; Dilarity 75.5%; Pred. No. 0.24 Conservative 0; Mismatches
                           Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                   JACOBSON, PRICE, HOLMAN &
                                                                                                                                                                                                                         Sequence 13, Application US/09385028 Patent No. 6232106
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Patent No. 6232106
GENERAL INFORMATION:
APPLICANT: Susan E. Jensen
APPLICANT: Kwamena A Aidoo
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MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
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1 Similarity 75.5%;
37; Conservative (
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               SEQUENCE CHARACTERISTICS:
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                                                                                                                                                                                                                                                                                                                                                                                                                                               CORRESPONDENCE ADDRESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                             NUMBER OF SEQUENCES:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Linear
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Best Local Similarity
Matches 37; Conserv
    Best Local Similarity
                                                                                                                                                                                                                                                                       GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STATE: D.C.
COUNTRY: U.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           20004
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADDRESSEE:
                                                                                                                                                                                                     US-09-385-028-13
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                      Atches
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Length 15079;

DB 4;

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LENGTH: 4411529
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                                                                                                                                                                                                                                                                                                                                                                                        TYPE: DNA
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                                                                                                                Score 26; DB 4; Length 1964;
Pred. No. 3.5;
0; Mismatches 15; Indels
                                                                                                                                                                                                     1 gacgagetgetggeggegetegggtacaaggtgegegeeteegacatgge 50
                                                                                                                                                                                                                                                                                                                                  GENERAL INFORMATION:
APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT
FILE REFERENCE: CL-1128-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: MCGONIGLE, BRIAN
APPLICANT: O'KEEF, DANIEL
TITLE OF INVENTION: PLANT GLUTATHIONE-S-TRANSFERASE ENZYMES
FILE REFERENCE: C1-1128-A
CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
BARLIER PILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DB 3;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           DB 3;
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Pred. No. 4;
                                                                                                                                                                                                                                                                                                                                                                                                                CURRENT APPLICATION NUMBER: US/09/248,335
CURRENT FILING DATE: 1999-02-10
EARLIER APPLICATION NUMBER: 08/924,759
EARLIER FILING DATE: 1997-September-05
NUMBER OF SEQ ID NOS: 74
SOFTWARE: Microsoft Word Version 7.0A
SEQ ID NO 39
LENGTH: 773
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      RESULT 6
US-09-248-335-53
; Sequence 53, Application US/09248335
; Patent No. 6096504
; GENERAL INPORMATION:
                                                                                                                                                                                                                                                                                                   Sequence 39, Application US/09248335 Patent No. 6096504
                               TYPE: DNA
; ORGANISM: Arabidopsis thaliana
US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    50.68;
73.38;
                                                                                                                51.0%;
70.0%;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ch 50.6%;
1 Similarity 73.3%;
33; Conservative
                                                                                                                                  Best_Local Similarity 70.0
Matches 35; Conservative
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Best Local Similarity
Matches 33; Conserv
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SEQ ID NO 1
LENGTH: 1964
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US-09-248-335-39
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
                                                                                                                                       APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: FLEISCHMAN, Robert D.
APPLICANT: WHITE, Owen R.
APPLICANT: FRASER, Claire M.
APPLICANT: FRASER, Claire M.
APPLICANT: Track Conversed to the conversed
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APPLICANT: WHITE, Owen R.
APPLICANT: WHITE, Owen R.
APPLICANT: FASSEN, Claire M.
APPLICANT: VENTER, John C.
TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM
TITLE OF INVENTION: TUBERCULOSIS
FILE REPERENCE: 24366-20007.00
CURRENT APPLICATION NUMBER: US/09/103,840A
CURRENT FILING DATE: 1998-06-24
NUMBER OF SEQ ID NOS: 2
SOFTWARE: PATENTIN VET. 2.1
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Pred. No. 7.4;
0; Mismatches 15; Indels 0;
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Pred. No. 7.4;
0; Mismatches 15; Indels 0;
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COTHER INFORMATION: H37Rv
US-09-103-840A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ORGANISM: Mycobacterium tuberculosis FEATURE:
Sequence 2, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/09103840A Patent No. 6294328 GENERAL INFORMATION:
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Best Local Similarity 69.4%;
Matches 34; Conservative 0
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Best Local Similarity 69.4%;
Matches 34; Conservative
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0; Mismatches Pred. No. 4;

33; Conservative

Best Local Similarity Matches 33; Conserv

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TITLE OF INVENTION: CARBAMOYL-PHOSPHATE SYNTHETASE GENE OF CORYNEFORM TITLE OF INVENTION: BACTERIA AND METHOD FOR PRODUCING L-ARGININE FILE REFERENCE: OP945CIP
CURRENT APPLICATION NUMBER: US/09/629,616
CURRENT FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 7
SOFTWARE: PATENTIN Ver. 2.0
SEQ ID NO 1
LENGTH: 4837
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICANT: Granneman, James G.
APPLICANT: Lahners, Kristine N.
APPLICANT: Lahners, Kristine N.
APPLICANT: Rac, Donald D.
TITLE OF INVENTION: @ @3-ADRENBEGIC RECEPTOR PROTEIN AND DNA
TITLE OF INVENTION: ENCODING SAME
NUMBER OF SEQUENCES: 9
ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &
ADDRESSEE: MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                             DB 4; Length 4837;
                                                                                                                                                                                                                                                                                                                                                                                                                             Score 24.4; DB 4; Length 4 Pred. No. 11; 0; Mismatches 11; Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390 CITY: Troy STATE: Michigan
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTKI: J. 48099

ZIF: 48099

COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC.DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/916,901

TITING DATE: 19920720
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CLASSIFICATION: 435
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-324(WSU)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3354
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
TENGTH: 2005 base pairs
                                                                                                                                                                                                         TYPE: DNA ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     US-07-916-901-5/c
; Sequence 5, Application US/07916901
; Patent No. 5364772
; GENERAL INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                             Query Match 47.8%;
Best Local Similarity 73.8%;
Matches 31; Conservative
                                                                                                                                                                                                                                                 ; FEATURE:
; NAME/KEY: CDS
; LOCATION: (283)..(1461)
; NAME/KEY: CDS
; LOCATION: (1470)..(4808)
US-09-629-616-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LOCATION:
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0
                                                                                                               APPLICANT: Philippsen, Peter
APPLICANT: Poliman, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
NUMBER OF SEQUENCES: 1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DB 4; Length 812;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 168 AGGACCTGATGCCGTCGCTGGAGAGATGCACGTCTCGTCCATTGCG 217
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       2 acgagetgetggeggegetegggtacaaggtgegegeetecgacatggeg 51
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Indels
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PF/5-30306/A/CGC1976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             47.8%; Score 24.4; DB
68.0%; Pred. No. 11;
tive 0; Mismatches
                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                              Sequence 401, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       US-09-629-616-1
; Sequence 1, Application US/09629616
; Patent No. 6255086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF,
TELECOMMUNICATION:
TELEPHONE: 919-541-8587
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 401:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
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NAKAMATSU, Tsuyoshi
KURAHASHI, Osamu
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 812 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Query Match
Best Local Similarity 68.0
Matches 34; Conservative
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                                                                                                                                                                                                                                                                                                                  NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62392
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US-08-998-416-401
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                                                                                               GENERAL INFORMATION:
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                              JS-08-998-416-401
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APPLICANT:
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APPLICANT: WHITE, OWEN R.

APPLICANT: FRASER Claire M.

APPLICANT: FRASER Claire M.

TITLE OF INVENTION: DNA SEQUENCES FOR STRAIN ANALYSIS IN MYCOBACTERIUM

TITLE OF INVENTION: TUBRECULOSIS

FILE REFERENCE: 24366-20007.00

CURRENT APPLICATION NUMBER: US/09/103,840A

CURRENT FILING DATE: 1998-06-24

NUMBER OF SEQ ID NOS: 2

SOUTWARE: PATENTIN Ver. 2.1

SEQ ID NO 2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ; OTHER INFORMATION: CDC 1551
; OTHER INFORMATION: "n" bases at various positions throughout the sequence
; OTHER INFORMATION: represent a, t, c or g
US-09-103-840A-2
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                                                                   Score 24; DB 1; Length 2005; Pred. No. 14;
                                                                                                                       Indels
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APPLICANT: EVANS, RONALD M.
APPLICANT: MANGELSDORF, DAVID J.
TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND
TITLE OF INVENTION: METHODS
NUMBER OF SEQUENCES: 7
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             1 gacgagetgetggeggegetegggtacaaggtgegegeeteegaea 46
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION UNMEER: US/08/336,408B
FILING DATE: 08-NOV-1994
                                                                                                                                                                    6 gctgctggcggcgctcgggtacaaggtgcgcgcctccgac 45
                                                                                                                                                                                                  131 GETGTTGGCTGCACTGGGGTCCAAGGTGGGGGGCGTCTGAC 92
                                                                                                                    0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ORGANISM: Mycobacterium tuberculosis
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COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
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                                                                                                                                                                                                                                                                                                                                      Sequence 2, Application US/09103840A Patent No. 6294328
                                                                     47.1%;
75.0%;
                                                                     Query Match 47.1
Best Local Similarity 75.0
Matches 30; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ZIP: 90071
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
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USA
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TYPE: DNA
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US-08-336-408B-1
US-07-916-901-5
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PCT-10591-01
PCT-10591-01
Sequence 1, Application PC/TUS9100399
GENERAL INFORMATION:
APPLICANT: Mangelsdorf, Dr., David J.
APPLICANT: Evans Dr., Ronald M.
TITLE OF INVENTION: RETINOID RECEPTOR COMPOSITIONS AND TITLE OF INVENTION: MTHODS
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             SOFTWARE PATENTIN STATEM: CONTROLL SOFTWARE PATENTIN Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/00399
FILING DATE: 19910122
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: 07.478,071
FILING DATE: 09-FEB-1990
ATTONNEY/AGENT INPOMBER: 09-FEB-1990
ATTONNEY/AGENT INPOMBER: STATEM NAME: REGISTRATION NUMBER: 31192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDESSEE: FITCH, EVEN, TABIN & FLANNERY STREET: 135 South LaSalle Street, Suite 900 CITY: Chicago STATE: Illinois COUNTRY: USA LIP: 60603 COMPUTRY READABLE FORM: MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: IBM PC COMPATIBLE COMPUTER: PROPERATING SYSTEM: PC-DOS/MS-DOS
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 07/933,453
FILING DATE: 21-AUG-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: WO PCT/US91/00399
FILING DATE: 22-AN-1991
PRIOR APPLICATION NUMBER: WO PCT/US91/00399
FILING DATE: 29-EEB-1990
ATTORNEY/AGENT INFORMATION:
NAME: REITER, STEPHEN E.
REGISTRATION NUMBER: 941 9851
TELECOMMUNICATION INFORMATION:
TELEFAX: 619-546-1995
INFORMATION FOR SEQ ID NO: 1:
SUMMUNICATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         0; Mismatches
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Query Match 45.9%; Score 23.4; Best Local Similarity 67.3%; Pred. No. 22; Matches 33; Conservative 0; Mismatches
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REFERENCE/DOCKET NUMBER: 50852
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (619) 552-131
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             LENGTH: 1866 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid STRANDEDNESS: both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         76..1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             both
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             NAME/KEY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ; LOCATION:
US-08-336-408B-1
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Pred. No. 22;
0; Mismatches 16; Indels 0
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APPLICANT: DELLAPORTA, STEPHEN L.
TITLE OF INVENTION: MATERIALS AND METHODS FOR PRODUCING
TITLE OF INVENTION: PLANTS WITH SINGLE-SEX FLOWERS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORTSON & FORESTER
STREET: 2000 PENNSTLVANIA AVE. N.W.
CITY: WASHINGTON
STATE: D.C.
COUNTRY: USA
COUNTRY: USA
CONPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PAPENTEN PC-DOS/MS-DOS
SOFTWARE: PAPENTEN PS-SOFTWARE: PS-SOFTW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        DB 1; Length 1236;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1 gacgagetgetggeggegetegggtacaaggtgegegeetecgacatgg 49
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1, Application US/08440856A Patent No. 5750873
TELEFAX: (619) 552-0095
TELEX: 20 6566 PATLAW CGO
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1866 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: single
TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
IMMEDIATE SOUNCE:
CLONE: RXR HUMAN ALPHA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX: (202) 887-0763
TELEX: 706141
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 1236 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Query Match
Best Local Similarity 67.3%;
Matches 33; Conservative
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   CDS
join(76..1464)
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STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; NAME/KEY:
; LOCATION:
PCT-US91-00399-1
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Search completed: December 19, 2001, 21:44:58 Job time: 11445 sec

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-MODEL-frame+_p2n.model_-DEW-x1p
-Q-/cgn2_1/USPTO_spool/US0948529/runat_19122001_165005_14373/app_query.fasta_1.77
-Q-/cgn2_1/USPTO_spool/US0948529/runat_19122001_165005_14373/app_query.fasta_1.77
-Q-/cgn2_1/USPTO_spool/US0948529/runat_1912001_165005_14373/app_query.fasta_1.77
-GAPEXT-4.000 -MINMATCH=0.100 -LOOPCL-0.000 -LOOPEXT-0.000
-GAPEXT-4.000 -MINMATCH=0.100 -LOOPCL-0.000 -YGAPEXT-0.500
-FGAPEXT-7.000 -YGAPOP-10.000 -YGAPEXT-0.500
-DELOP-6.000 -DELEXT-7.000 -START-1 -MATRIX-blosum62
-TRANS-human40.cdi -LIST-1000 -DCCALIGN-200 -THR_SCORE-pct
-TRANS-human40.cdi -LIST-1000 -DCCALIGN-200 -THR_SCORE-pct
-TRANS-human40.cdi -LIST-1000 -NDCALIGN-200 -THR_SCORE-pct
-TRANS-human40.cdi -LIST-1000 -ALIGN-50 -MODE-LOCAL -OUTFMT-pfs
-NORM-ext -MINLEN-0 -MAXLEN-2000000000
-USER-US08485529_GCGN1_1_248 -NCPU-6 -ICPU-3 -LONGLOG -NO_XLDXY
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Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36263
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Richards DE;
                                to: AAX36284 from: 1
                                                                                                                                                                                                           seq_documentation_block:
ID AAX36263 standard; DNA; 453 BP
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    US-09-485-529-104 x AAX36284
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1.5e+06
1.7e+06
1.9e+06
1.9e+06
591.93
691.86
                                                                                                    1.2e+03
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   41.61
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/SIDS2/gcgdata/geneseqn/NA2000.DAT:AAI32864+
                                                                                                                                                                                                                                                                                                                 Oligonucleotide derived from the wheat rht gene.
    /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH68530
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Richards DE;
                                                                                                                                                                                                     Claim 3; Page 53; 88pp; English.
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Ratio: 4.765
Percent Similarity: 100.000
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its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by globerallin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with globerallin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerallin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit globerallin blosynthesis, such as paclobutazol, e.g. to allow use of a gibberallin blosynthesis inhibitor to keep weeds obtained after partially commend. The present sequence was
The specification describes polypeptides encoded by the Rht gene (and
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Ratio: 4.765
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Thu Dec

US-09-485-529-104 x AAX36263

to: 2125

from: 1

to: AAX36279

Align seg 1/1

US-09-485-529-104 x AAX36279

alignment_block

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Trilicum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants wild-type, the dwarfing out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents the wheat Rht clone 5al genomic sequence.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36279
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 17
Gaps: 0
Percent Identity: 100.000
   to: 453
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Wheat Rht clone 5al genomic sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DE;
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       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                    sed_documentation_block:

XX
AAX36279;
XX
AAX36279;
XX
T16-JUL-1999 (first entry)
XX
Wheat Rht clone 5al genomic seq
XX
Wheat Rht clone 5al genomic seq
XX
Wheat Rht clone 5al genomic seq
XX
XX
Rht gene; homologue; Triticum a
Antagonist; gibberellin; dwarf |
XX
AC111cum aestivum.
XX
WO990174-Al.
XX
C7-AUG-1999; 97GB-0017192.
XX
C7-AUG-1999; 97GB-0017192.
XX
X 25-FEB-1999.
XX
X 711cum Aestivum polynucle
XX
XX
WPI; 1999-181040/15.
PT
Harberd NP, Peng J, Richards SX
XX
WPI; 1999-181040/15.
DR
YY
New Triticum Aestivum polynucle
PT
Antagonised by gibberellin, use
XX
New Triticum Aestivum polynucle
PT
Antagonised by gibberellin, use
XX
New Triticum Aestivum polynucle
PT
Antagonised by gibberellin, use
XX
New Triticum Aestivum polynucle
PT
Antagonised by gibberellin, use
XX
Antagonis
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Ratio: 4.765
Percent Similarity: 100.000
to: AAX36263
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   Align seg 1/1
                                                                                                                                                                                                                                                                                                             323 G 323
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the composite DNA sequence of wheat Rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                        pmologue; Triticum aestivum; wheat; growth inhibition;
glibberellin; dwarf phenotype; glibberellin biosynthesis;
seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 2709 BP; 473 A; 900 C; 823 G; 482 T; 31 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 17
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                        Composite DNA sequence of wheat Rht gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Disclosure; Fig 3a; 88pp; English.
                                                                                                                                                                                                BP
                                                                                                                                                                                               AAX36275 standard; DNA; 2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BIOSCIENCE LTD.
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                                                                                                                                                                                                                                                                   16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 81.00
Ratio: 4.765
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Harberd NP, Peng J,
                                                                                                                                                                                                                                                                                                                                          Rht gene; homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 1999-181040/15.
                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                Triticum aestivum.
                                                                                                                                                                                                                                                                                                                                                                                 paclobutrazol; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (PLAN-) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9909174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                            antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        25-FEB-1999
                                                                                                         189 G 189
                                                                                                                                                                                                                                    AAX36275;
                                                                      17 a 17
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alignment_block:
US-09-485-529-104 x AAX36281
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      gene; homologue; Triticum aestivum; wheat; growth inhibition; igonist; glbberellin; dwarf phenotype; glbberellin blosynthesis;
                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36281
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 302 BP; 52 A; 82 C; 123 G; 45 T; 0 other;
                                                                                              to: 2709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Partial sequence of the maize D8-1 allele.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Triticum Aestivum polynucleotides
provides inhibition of the growth of p
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Disclosure; Fig 11a; 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Harberd NP, Peng J, Richards DE;
                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           AAX36281 standard; DNA; 302 BP
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                              US-09-485-529-104 x AAX36275
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         paclobutrazol; maize; ss
                                                                                              Align seg 1/1 to: AAX36275
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P-PSDB; AAY02542.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           antagonist;
alignment_block:
                                                                                                                                                                                                                                                                                                                                                            323 G 323
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     AAX36281;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by growth of the plant. This growth inhibition is antagonised by alounts. Conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with used to produce Rht mutant plants which are dwarfed compared with may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as paclobutrazol, compounds which inhibit gibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the maize D8-2023 allele.
                                                                                                                                                                                                                                                                                                                                                                        Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; maize; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                     100 GATGAGCTGCCGCGCTCGGGTACAAGGTGCGTTCGTCGATATGGC 149
                                   1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36282
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Sequence 371 BP; 56 A; 121 C; 139 G; 55 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17
                                                                                                                                                                                                                                                                                                                                          Partial sequence of the maize D8-2023 allele.
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Gaps:
to: 302
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to: AAX36281 from: 1
                                                                                                                                                                                                                                    BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANT BIOSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            98WO-GB02383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97GB-0017192.
                                                                                                                                                                                                                seq_documentation_block:
ID AAX36282 standard; DNA; 371
                                                                                                                                                                                                                                                                                                         16-JUL-1999 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              78.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    WPI; 1999-181040/15.
P-PSDB; AAY02543.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Harberd NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         25-FEB-1999
Align seg 1/1
                                                                                                                                             150 G 150
                                                                                                                                                                                                                                                                                                                                                                                                                                                      Zea mays.
                                                                                                                                                                                                                                                                       AAX36282;
                                                                                                         17 a 17
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Ratio:

Length: 17 Gaps: 0 Percent Identity: 94.118

Quality: 78.00 Ratio: 4.588 Percent Similarity: 100.000

alignment_scores:

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberelin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologus gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis, such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence represents the expressed sequence tag (EST) AAD39460, which is homologous to the
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; rice; expressed sequence tag; EST; ss.
                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36277
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Rice EST D39460 sequence, homologous to wheat Rht gene.
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    Percent Identity: 94.118
                                                                                                                                                                                                     to: 371
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XX
AAX36277;
XX
AAX36277;
XX

16-JUL-1999 (first entry)
XX
Shift gene; homologue; Triticum aes antagonist; gibberellin; dwarf ph paclobutrazol; rice; expressed segressed set of the pack of the pac
                                                                                                                                                                                                     from: 1
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                                                                           alignment_block:
US-09-485-529-104 x AAX36282
                                                                                                                                                                                                 to: AAX36282
Percent Similarity: 100.000
                                                                                                                                                                                                     Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                114 G 114
                                                                                                                                                                                                                                                                                                                                                                                                                                                17 a 17
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alignment_scores:

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its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as pacibutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the maize lal genomic clone sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           The specification describes polypeptides encoded by the Rht gene (and
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     which
is
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         homologue; Triticum aestivum; wheat; growth inhibition; ;; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     New Triticum Aestivum polynucleotides - encode a polypeptide provides inhibition of the growth of plants, which inhibition antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                  114 GACGAGCTGCTGGCGCTCGGGTACAAGGTGCGGTCGTCCGACATGGC 163
                                                                                                                                                              1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                         seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36280
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 Length: 17
Gaps: 0
Percent Identity: 94.118
                                                                                                                          to: 770
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Disclosure; Fig 9a; 88pp; English.
                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Maize lal genomic clone sequence.
                                                                                                                                                                                                                                                                                                                                            seq_documentation_block:
ID AAX36280 standard; DNA; 2255 BP
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                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              paclobutrazol; maize; ss
                                                                        alignment_block:
US-09-485-529-104 x AAX36277
                                                                                                                            to: AAX36277
Quality: 78.00
Ratio: 4.588
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             antagonist;
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                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              dene;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Zea mays.
                                                                                                                                                                                                                                                                        164 C 164
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                                                                                                                                                                                                                                    17 a 17
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin blosynthesis, such as pacloburrazol, e.g. to allow use of a gibberellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial cDNA sequence of rice AAD39460 (a wheat Rht gene homologue).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; glbberellin; dwarf phenotype; glbberellin blosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Partial cDNA sequence of rice D39460 (a wheat Rht gene homologue).
                                                                                                                                                                                                             1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36276
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               Length: 17
Gaps: 0
Percent Identity: 94.118
                                                                                                                                                    to: 2255
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                                                                                                                                                    from: 1
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ID AAX36276 standard; DNA; 725 BP
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                                                                                         alignment_block:
US-09-485-529-104 x AAX36280
             Quality: 78.00
Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                  Align seg 1/1 to: AAX36280
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paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Oryza sativa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         W09909174-A1
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alignment_scores
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                                                                                                                                                                                                                                                                                                       358 G 358
                                                                                                                                                                                                                                                                                                                                                                                                                                         AAX36276;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Trilicum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by globerellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the treatment with globerellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being globerellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit globerellin blosynthesis, such as paclobutrazol, e.g. to allow use of a globerellin blosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was contained after partially sequencing wheat Rht clone 5al.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence obtained after sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                                                                                                                                                                               109 GAGCTGCTGGCGCGCTCGGGTACAAGGTGCGGTCGTCCGACATGGCC 156
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36273
                                                                                                                                                                                                                                                                                                                                                                        2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
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Gaps: 0
Percent Identity: 100.000
                           Length: 16
Gaps: 0
Percent Identity: 93.750
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ID AAX36273 standard; DNA; 324 BP.
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US-09-485-529-104 x AAX36276
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Percent Similarity: 100.000
                                                                 Ratio: 4.500
Percent Similarity: 100.000
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Ratio:
                                  Quality:
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alignment_scores
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seq_documentation_block:
ID AAC45745 standard; DNA; 1602
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99US-0132486.
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alignment_block:
US-09-485-529-104 x AAC65312
                                                                                        Align seg 1/1 to: AAC65312
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      The present sequence is given in a specification relating to the structure and function of a regulatory gene, SCARECROW (SCR).

SCARECROW-like (SCL) genes encoding proteins containing an amino acid sequence similar to the sequence of MOTIF III (VHIID) of Arabidopsis SCR protein are disclosed. SCR and SCL genes are useful for producing transgenic plants whose cell division is modified and root and/or stem development and gravitropism of stem or hypocotyl is altered. Cell division is increased or decreased in roots resulting in thicker or finance root development. The transgenic plants are useful for expressing a gene of interest encoding a gene product that confers herbicide, salt, pathogen or insect resistance in root or embryos and genes encoding starch, lighth or cellulose biosynthesis in shoots. The SCR gene also confers less susceptibility to lodging in the transgenic plants than a wild-type plant. SCR gene sequences are also useful as molecular markers in the sequence are also useful as molecular markers.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Scarecrow gene; SCR gene; plant; regulatory gene; SCARECROW-like; SCL; transgenic plant; cell division; molecular marker; herbicide resistance;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Scarecrow gene useful for producing transgenic plants expressing genes whose product increases starch, lignin or cellulose biosynthesis and confers herbicide, pathogen or insect resistance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Ë
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Pysh
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 salt resistance; pathogen resistance; insect resistance; ss.
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                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC65312
                                                                                                                                                                       Align seg 1/1 to reverse of: AAX36273 from: 1 to: 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 457 BP; 141 A; 86 C; 87 G; 125 T; 18 other;
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Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Claim 6; Fig 28M; 200pp; English.
                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:

XX
AAC65312 standard: CDNA; 457 BP
XX
AAC65312;
XX
O9-FEB-2001 (first entry)
XX
Scarecrow gene; SCL EST 722782.
XX
Scarecrow gene; SCR gene; plant
XX
WC200053723-A2.
XX
Arabidopsis thaliana.
XX
WO200053723-A2.
XX
Arabidopsis thaliana.
XX
WO200053723-A2.
XX
ACCOCC 2000WO-US05875.
XX
O7-MAR-1999; '99US-0265585.
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O7-MAR-1999; '99US-0265585.
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UVNY ) UNIV NEW YORK STATE.
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WPI; 2000-594315/56.
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COTHER STATE.
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CONFERS PREDICTION OF A reg
CC SCARECROW-like (SCL) genes enco
CC GC SCARECROW-like (SCL) genes enco
CC GON GENES SCARE GOLD
CC GON GENES SCARE GOLD
CC GON GENES SCARE 
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Y, Bruce W, Lim J;
                                                     US-09-485-529-104 x AAX36273/rev
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Ratio: 4.118
Percent Similarity: 100.000
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                            alignment_block:
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control;
                 1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC45745
                                                                                                                  Hybridisation assay; genetic mapping; gene expression protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
                                                                                                       Arabidopsis thaliana DNA fragment SEQ ID NO: 47609.
to: 457
from: 1
                                                                                                                                                                                                                                                                                                                                                                                      99US-0137222
99US-0137528
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	Length:
\(\frac{1}{2}\) \(\frac{1}\) \(\frac{1}{2}\) \(\frac{1}{2}\) \(\frac{1}{2}\) \(\frac{1}{2}\) \(\frac{1}{2}\) \	ty: 70.00
PR 06-AUG-1999; PR 06-AUG-1999; PR 09-AUG-1999; PR 09-AUG-1999; PR 10-AUG-1999; PR 11-AUG-1999; PR 11-AUG-1999; PR 11-AUG-1999; PR 11-AUG-1999; PR 12-AUG-1999; PR 20-AUG-1999; PR 21-AUG-1999; PR 21-AUG-1999; PR 21-AUG-1999; PR 22-AUG-1999; PR 22-AUG-1999; PR 22-AUG-1999; PR 22-AUG-1999; PR 22-AUG-1999; PR 22-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999; PR 22-AUG-1999; PR 23-AUG-1999; PR 23-AUG-1999; PR 21-OCT-1999; PR 22-CCT-1999; PR 23-CCT-1999; PR 23-CCT-1999	Quality
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4440\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\\	
990S-0137724. 990S-0137724. 990S-0137724. 990S-0138447. 990S-0138447. 990S-0139452. 990S-0139452. 990S-0139455. 990S-0139455. 990S-0139455. 990S-0139455. 990S-0139455. 990S-0139455. 990S-0139455. 990S-0139455. 990S-0139463. 990S-0139463. 990S-014834. 990S-014834. 990S-014834. 990S-014834. 990S-014834. 990S-014433. 990S-0144334. 990S-0145289.	908
	AUG-199
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us-09-485-529-104.p2n.rng

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cactors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control superts of physiology, metabolism and development. Therefore the cDNAs and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, response, wounding response, cell cycle regulation, pathogen response, wounding response, cell cycle regulation, pathogen response, wounding response, cell cycle regulation, pagnetations, plants in seeds, tubers, roots, and other storage organs leading to an increase in yield. The transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, conion, papaya, peas, pepers, pineapple, spinach, squash, sweet corn, tobacco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Transcription factor; biochemical characteristic; controlling element; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology; plant trait modification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/genesegn/NA2001.DAT:AAD05776
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Transcription factor, G307"
                                                                                                                                                                                                                                                                                                                                 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana transcription factor, G307 cDNA.
                                                                                                                                                                                                                                                                                                                                                                                         Length: 17
Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                               Sequence 1764 BP; 431 A; 383 C; 448 G; 502 T; 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 1764
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1..1764
/*tag= a
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ID AAD05776 standard; cDNA; 1764 BP
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2000US-0197899.
2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    31-JUL-2001 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-485-529-104 x AAD06661
                                                                                                                                                                                                                                                                                                                                                                                                           Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: AAD06661
                                                                                                                                                                                                                                                                                                                                                                                           70.00
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                                                                                                                                                                                                                                                                                                                                                                                              Quality:
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17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                   factor cDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   25-MAY-2001
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Plant transcription factor; phenotype; sugar sensing characteristic; transgenic plant; plant yield; growth; germination; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; planeatation; flowering; senescence; physiology; storage organ; metabolism; sa
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 polypeptides, useful plants and increasing
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The patent relates to polynucleotides encoding 35 plant transcription
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Heard J, Pineda O, Pilgrim M, Adam L, Riechmann JL;
                                                                                                                           A. thaliana transcription factor G308 homolog, G307 cDNA.
                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/genesegn/NA2001.DAT:AAD06661
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /product= "Transcription factor homolog"
       Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Nucleic acids encoding plant transcription factor for altering the sugar sensing characteristics of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 yield, e.g. corn, potato and cotton plants -
                                                                                               to: 1602
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Claim 4; Page 113-115; 151pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers 1.1764
                                                                                                 from: 1
                                                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAD06661 standard; cDNA; 1764 BP.
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17-APR-2000; 2000US-0197899.
22-AUG-2000; 2000US-0227439.
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                                                                                                                                                                                                                                                                                                                                                            10-AUG-2001 (first entry)
                                                 alignment_block:
US-09-485-529-104 x AAC45745
    Ratio: 4.118
Percent Similarity: 100.000
                                                                                               Align seg 1/1 to: AAC45745
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Arabidopsis thaliana.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              PINEDA O.
PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           SAMAHA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    P-PSDB; AAE02560.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Samaha R;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADAM L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            WO200135725-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           25-MAY-2001
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(RIEC/)
(YUGG/)
(SAMA/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 HEAR/)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ľu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Key
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Plant transcription factor; phenotype; sugar sensing characteristic;

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The present sequence is Arabidopsis thaliana transcription factor, G307 cDNA. The transcription factor is used for altering a plant's blochemical characteristics. The transcription factor may be used to blochemical characteristics of plants be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, sunflower, alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onion, papaya, peas, peppers, plneaple, spinach, squash, sweet corn, tobacco, tomato, watermelon, cosaceous fruits and/or vegetable brassicas. Transcription factors are key controlling alements of biological pathways and altering expression levels of or more transcription factors can change entire biological pathways in an organism. Therefore manipulating transcription factor fevels in plants offers great potential in agricultural biotechnology for modifying a plant's traits. Transcription factor cDNA is useful in
                                                                                                                                                                                                                                                                                                             Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn,
                                                                                                                                                                                                       Riechmann JL, Heard J, Samaha R;
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/genesegn/NA2001.DAT:AAD06646
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Sequence 1764 BP; 431 A; 383 C; 448 G; 502 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length:
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                                                                                                                                                                                                                                                                                                                                                                                Claim 4; Page 66-68; 127pp; English.
                MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                           Adam L, )
), Jiang (
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAD06646 standard; cDNA; 1951
                                                                                                                                                                                                                                                                                                                                                 potato and cotton plants -
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Percent Similarity: 100.000
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                                                                  ADAM L.
RIECHMANN J L.
                                                                                                                                                                                                           Yu G, Ad
Pineda O,
                                                                                                                                                                                                                                                             WPI; 2001-335999/35
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                                CREELMAN R.
                                                                                                                                    PILGRIM M.
PINEDA O.
                                                                                                    HEARD J.
SAMAHA R.
                                                                                                                                                                                                                                                                           P-PSDB; AAE01892
                                                                                                                                                                        JIANG C.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment block;
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(PINE/)
(JIAN/)
                 MEND-)
                                CREE/
                                                                                                    HEAR/
                                                                  ADAM/
                                                                                    RIEC/
                                                                                                                      SAMA/
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XEXEXEX
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The patent relates to polynucleotides encoding 35 plant transcription factors which may be used to modify phenotype associated with a plant's sugar sensing characteristics and increasing yield when their expression level is altered. Sugars are central regulatory molecules that control aspects of physiology, metabolism and development. Therefore the CDNAs and proteins of the invention are useful for modifying the growth and germination rates of plants, photosynthesis, glyoxylate metabolism, response, wounding response, cell cycle regulation, pathogen response, wounding response, cell cycle regulation, pathogen relationships in seeds, tubers, roots, and other storage organs leading to an increase in yield the transcription factor polynucleotides and polypeptides may be used to alter the structure and developmental characteristics of plants such as soybean, wheat, corn, potato, cotton, rice, oilseed, sunflower, alfalfa, sugarcane, turf, banana, blackberry, collee, cucumber, eggplant, grapes, honey dew, lettuce, mango, meton, of the plants, peas, peas, peppers, plicapple, spinach, squash, seet, con, onlon, papaya, peas, peppers, plicapple, spinach, squash, seet, con,
            transgenic plant; plant yield; growth; germination; photosynthesis; glyoxylate metabolism; respiration; pathogen response; wounding response; cell cycle regulation; pigmentation; flowering; senescence; physiology;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            acco, tomato, watermelon, rosaceous fruits and/or vegetable brassicas. present sequence is an Arabidopsis thaliana transcription factor
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Nucleic acids encoding plant transcription factor polypeptides, useful for altering the sugar sensing characteristics of plants and increasing yield, e.g. corn, potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Riechmann JL;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Sequence 1951 BP; 482 A; 419 C; 475 G; 575 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Pineda O, Pilgrim M, Adam L,
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                                                                                                                                                                    /*tag= a
/product= "Transcription factor"
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Gaps:
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                                                                                                                                  Location/Qualifiers
196..1794
                                                                                                                                                                                                                                                                                                                                                                                 MENDEL BIOTECHNOLOGY INC.
                                                                storage organ; metabolism; ss
                                                                                                                                                                                                                                                                                   14-NOV-2000; 2000WO-US31414
                                                                                                                                                                                                                                                                                                                                    2000US-0197899
2000US-0227439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   70.00
4.118
                                                                                               Arabidopsis thaliana.
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YU G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      WPI; 2001-335977/35.
P-PSDB; AAE02545.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Jiang C, Heard J,
Yu G, Samaha R;
                                                                                                                                                                                                                                                                                                                                                                                                                                    PINEDA O.
PILGRIM M.
                                                                                                                                                                                                                                                                                                                                                                                                      JIANG C.
HEARD J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SAMAHA R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ADAM L.
                                                                                                                                                                                                                    WO200135725-A1
                                                                                                                                                                                                                                                                                                                                    17-APR-2000;
22-AUG-2000;
                                                                                                                                                                                                                                                                                                                    17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                      25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 copacco,
                                                                                                                                                                                                                                                                                                                                                                                                                   (HEAR/)
(PINE/)
(PILG/)
(ADAM/)
(RIEC/)
                                                                                                                                                                                                                                                                                                                                                                                       (MEND-)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (SAMA/)
                                                                                                                                                                                                                                                                                                                                                                                                     (JIAN/)
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such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, such as soybean, wheat, corn, potato, cotton, rice, oilseed rape, standlower, alfalfa, sugar cane, turf, banana, blackberry, blueberry, strawberry, raspberry, cantaloupe, carrot, cauliflower, coffee, cucumber, eggplant, grapes, honey dew, lettuce, mango, melon, onlon, papaya, peas, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, peppers, pineapple, spinach, squash, sweet corn, tobacco, tomato, atterment, rasaccous fruits and/or vegetable brassicas Transcription factors are key controlling elements of biological pathways and altering expression levels of lor more transcription factors can change entire factor levels in plants offers great potential in agricultural biotechnology for modifying a plant's traits. Transcription factor cDNA
    to alter the structure and developmental characteristics of plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Nucleic acid encoding gibberellin inhibitor GAI and related antisense sequences – used to create tall, or particularly, dwarf plants, especially crops such as maize, rice and wheat
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gibberellin insensitivity, gai, plant growth inhibition, dwarf phenotype, lodging resistance, increased yield; flowering regulation; bolting inhibition; spinach, lettuce, antibody; identification; probe; primer; antisense; sense; expression regulation; co-suppression; rice; Bakane disease resistance; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT91937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Arabidopsis thaliana gibberellin insensitivty gene gai.
                                                                                                                                                                                                                                                                                            Sequence 1951 BP; 482 A; 419 C; 475 G; 575 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                              Length: 17
Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: 1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (INNE-) INNES CENT INNOVATIONS LTD JOHN,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AAT91937 standard; DNA; 1964 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97WO-GB00390.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     96GB-0002796
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     19-MAR-1998 (first entry)
                                                                                                                                                                                                                                                          is useful in gene therapy.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-485-529-104 x AAD05791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              to: AAD05791
                                                                                                                                                                                                                                                                                                                                                                                                                         Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                  70.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Carol P, Harberd NP,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Arabidopsis thaliana
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-415295/38
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               P-PSDB; AAW30792
                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                      Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            W09729123-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              12-FEB-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     12-FEB-1996;
                                                                                                                                                                                                                                                                                                                                                               alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     14-AUG-1997
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  aliqnment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                324 T 324
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAT91937;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 a 17
    used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              The present sequence is Arabidopsis thaliana transcription factor, G308 cDNA, a homologue of G307. The transcription factor is used for altering a plant's biochemical characteristics. The transcription factor may be
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Transcription factor; biochemical characteristic; controlling element; structural characteristic; developmental characteristic; gene therapy; agricultural biotechnology; plant trait modification; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleic acids encoding plant transcription factor polypeptides, useful for altering the biochemical characteristics of plants e.g. corn,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Samaha R;
                                                                                                                                                                      274 GATGAGCTTCTAGCTGTTCTTGGTTACAAGGTTAGGTCATCGGAAATGGC 323
                                                                                                                                              1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                  seq_name: /SIDS2/gcgdata/geneseq/genesegn/NA2001.DAT:AAD05791
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /*tag= a
/product= "Transcription factor, G308"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Riechmann JL, Heard J,
C;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Arabidopsis thaliana transcription factor, G308 cDNA.
    Percent Identity: 82.353
                                                                                                       to: 1951
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Claim 4; Page 112-113; 127pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
196..1794
/*tag= a
                                                                                                       from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           (MEND-) MENDEL BIOTECHNOLOGY INC.
                                                                                                                                                                                                                                                                                                                                                           _documentation_block:
AAD05791 standard; cDNA; 1951 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Adam L,
O, Jiang
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-APR-2000; 2000US-0197899
22-AUG-2000; 2000US-0227439
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0166228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                14-NOV-2000; 2000WO-US31344
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        potato and cotton plants -
                                                                                                                                                                                                                                                                                                                                                                                                                                                              31-JUL-2001 (first entry)
                                                     US-09-485-529-104 x AAD06646
                                                                                                       to: AAD06646
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 YU G.
ADAM L.
RIECHMANN J L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Pineda O,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Arabidopsis thaliana.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   WPI; 2001-335999/35.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Yu G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CREELMAN R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              HEARD J.
SAMAHA R.
PILGRIM M.
PINEDA O.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           P-PSDB; AAE01907
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  JIANG C
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200136597-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    17-NOV-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Creelman R,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Pilgrim M,
                                           alignment_block
                                                                                                       Align seg 1/1
                                                                                                                                                                                                                                                                       324 T 324
                                                                                                                                                                                                                                                                                                                                                                                                                     AAD05791;
                                                                                                                                                                                                                              17 a 17
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(SAMA/) (PILG/) (PINE/) (RIEC/) (HEAR/)

CREE/) (ADAM/) (XDGG/)

(JIAN/)

Tanguy X;

Froger N,

Barret P, Brunel D,

Delourme R,

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(INRG ) INRA INST NAT RECH AGRONOMIQUE.
Renard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   GRAS protein; BZH gene; transcription factor; gibberellin; morphogenesis; plant development; dwarf plant; crucifer; ss.
                                            insensitivity (gai) gene product (GAI), the expression of which inhibits plant growth. However the inhibition is antagonised by cibberellin (GA), while gai expression confers a dwarf phenotype that is insensitive to GA. Manipulating gai and GAI expression confers to produce tall or dwarf plants, particularly the latter for increased resistance to lodging and increased yield. It may also allow regulation of flowering, i.e. plants remain in the vegetative state until treated with GA, useful to inhibit bolting in spinach and lettuce. GAI can be used to raise specific antibodies for identifying homologous proteins or genes in other species. gai fragments can also be used as probes or primers to identify and colone related sequences, or in the preparation of antisense or sense expression regulating (co-suppressing) sequences. Rice plants that express GAI may be resistant to Bakane disease. Manipulation of gai and GAI makes it possible to tailor the degree of dwarfism
                                    The present sequence encodes the Arabidopsis thaliana gibberellin
                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF25480
                                                                                                                                                                                                                                                              Sequence 1964 BP; 489 A; 426 C; 474 G; 575 T; 0 other;
                                                                                                                                                                                                                                       and GA sensitivity to particular crops or situations
                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Nucleotide sequence of a wildtype GRAS protein.
                                                                                                                                                                                                                                                                                                                Length:
                                                                                                                                                                                                                                                                                                                                                                                                      to: 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   (INRG ) INRA INST NAT RECH AGRONOMIQUE.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
60..1778
/*tag= a
                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/product= "GRAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    BP
             Claim 2; Fig 3; 76pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAF25480 standard; DNA; 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  02-AUG-2000; 2000WO-FR02216
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          99FR-0010023
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     15-MAY-2001 (first entry)
                                                                                                                                                                                                                                                                                                             Quality: 70.00
Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                             US-09-485-529-104 x AAT91937
                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAT91937
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Brassica napus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 40200109356-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            02-AUG-1999;
                                                                                                                                                                                                                                                                                                    alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          08-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                  alignment_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       337 T 337
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAF25480;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               17 a 17
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GRAS protein; BZH gene; transcription factor; gibberellin; morphogeneals; plant development; dwarf plant; crucifer; ss.
                                                                                                                                                                                             The present sequence encodes a wild type plant protein of the GRAS family. The specification describes a mutant allele of the BZH gene, which contains a G1695A mutation resulting in the mutation E546K in the protein. GRAS proteins are transcription factors implicated in regulation of the response to gibberellins and thus in control of morphogenesis and plant development. The mutant GRAS protein is used to produce dwarf plants, specifically cruoifers. Dwarf plants may be sown earlier (increasing nitrate accumulation without risking excessive stem growth during winter), and have better resistance to cold and lodging. They are also easier to harvest and allow for better monitoring of the crop.
                                                                            а
                                                                    New mutant nucleic acid encoding modified GRAS family protein, used produce dwarf transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAF25481
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 1779 BP; 418 A; 430 C; 476 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Nucleotide sequence of a mutant GRAS protein.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 1779
                                                                                                                                                            Example 1; Page 13-15; 28pp; French.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Location/Qualifiers
60..1778
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AAF25480 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   "GRAS"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAF25481 standard; DNA; 1779
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                02-AUG-2000; 2000WO-FR02216.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product=
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
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US-09-485-529-104 x AAF25480
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 3.882
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      66.00
WPI; 2001-182964/18
                           P-PSDB; AAB31883
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Brassica napus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WO200109356-A1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                15-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         08-FEB-2001.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         233 T 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AAF25481;
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us-09-485-529-104.p2n.rng

Page 19

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65.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rht gene; homologue;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 1999-181040/15.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            paclobutrazol; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Triticum aestivum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          P-PSDB; AAY02544
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   antagonist;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    25-FEB-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAX36283;
     The present sequence encodes a mutant plant protein of the GRAS family. The mutant allele of the BZH gene contains a G1695A mutation resulting in the mutation E546K in the protein. GRAS proteins are transcription factors implicated in regulation of the response to gibberellins and thus in control of morphogenesis and plant development. The mutant GRAS protein is used to produce dwarf plants, specifically crucifiers. Dwarf plants may be sown earlier (increasing nitrate accumulation without risking excessive stem growth during winter), and have better resistance to cold and lodding. They are also easier to harvest and allow for better monitoring of the crop.
                                                                                                                                                           ç
                                                                                                                                                        encoding modified GRAS family protein, used
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                           Tanguy X;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36266
                           Froger N,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Sequence 1779 BP; 419 A; 430 C; 475 G; 455 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length: 17
Gaps: 0
Percent Identity: 76.471
                           Brunel D,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 1779
                                                                                                                                                                                                                              Example 1; Page 18-20; 28pp; French.
                        Barret P,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Harberd NP, Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: AAF25481 from: 1
                                                                                                                                                                                   produce dwarf transgenic plants
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANT BIOSCIENCE LTD
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              200
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality: 66.00
Ratio: 3.882
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAX36266 standard; DNA;
                                                                                                                                                        New mutant nucleic acid
                           Delourme R,
                                                                         WPI; 2001-182964/18
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        WPI; 1999-181040/15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              paclobutrazoľ; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 friticum aestivum.
                                                                                                    P-PSDB; AAB31884
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                        Renard M,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              233 T 233
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAX36266;
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants can be wild-type, the dwarfing being gibberellin-insensitive gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was contained after partially sequencing wheat Rht clone 14al.
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New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              mologue; Triticum aestivum; wheat; growth inhibition;
gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36283
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            79 GACTATCTGCTGGCGGCGCTCGGGTACAAGGTGCGCGCCTCCGAC 123
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 93.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Sequence 200 BP; 24 A; 58 C; 84 G; 27 T; 7 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Partial sequence of the wheat rht-10 allele.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 200
                                                                                                        Disclosure; Fig 2b(12); 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAX36283 standard; DNA; 416 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  4.643
93.333
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US-09-485-529-104 x AAX36266
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: AAX36266
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plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as pacibutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence represents the partial sequence of the wheat rht-10 allele.
                                                           The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              DNA sequence obtained after sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36261
                                                                                                                                                                                                                                                                                                                                                                                     Length: 13
Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                                                     Sequence 416 BP; 59 A; 168 C; 129 G; 60 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         5 AlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 GCGCCCTCGGGTACAAGGTGCGCCCTCCGACATGGCG 39
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: AAX36283 from: 1 to: 416
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Disclosure; Fig 2b(7); 88pp; English.
                             Fig 12a; 88pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x AAX36283
                                                                                                                                                                                                                                                                                                                                                                                    Quality: 62.00
Ratio: 4.769
Percent Similarity: 100.000
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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit: growth of the plant. This growth inhibition is antagonised by gibberallin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberallin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberallin-insensitive. Tabler plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberallin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberallin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. The present sequence was cobtained after partially sequencing wheat Rht clone 14al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  DNA encoding Hevea brasiliensis (S)-hydroxy:nitrilase - useful for production of cyanohydrin(s) from aldehyde and hydrogen cyanide
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (S)-hydroxynitrilase; production;(S)-cyanohydrin; aldehyde;hydrogen cyanide; recombinant;ss.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT86824
                                                                                                                                                                                                                                                                                                                      Sequence 309 BP; 47 A; 102 C; 102 G; 45 T; 13 other;
                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0 Gaps: 0 Percent Identity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 309
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           8 GlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      18 GGGTACAAGGTGCGCGCCTCCGACATG 44
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAX36261 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
ID AAT86824 standard; cDNA; 817 BP.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 95DE-1029116
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US-09-485-529-104 x AAX36261
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Percent Similarity: 100.000
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P-PSDB; AAW29164.
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Recombinant S-HN has higher specific activity

and ketone.

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8*888888888888888888888888
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high specific activity, for chiral synthesis of cyano:hydrin(s)
(S)-cyanohydrins from aldehyde and hydrogen cyanide. Recombinantly produced S-HN has higher specific activity than native S-HN, probably due to post translational modification differences between plants and microorganisms.

S-HN was isolated from H. brasiliensis leaves by homogenisation, followed by sequential chromatography on QAE-Sepharose FF, Phenyl-Sepharose and Biogel P180. A cDNA bank from the same source was prepared and screened with polyclonal rabbit antiserum raised against the isolated enzyme. The insert, about 1.1 kb, in the single positive clone was cloned into pHNLL00 and sequenced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       The present sequence encodes the Hevea brasiliensis
S-hydroxynitrilase (S-HN), which can be used for the chiral
synthesis of aliphatic or aromatic S-cyanohydrins from HCN, or its
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Schall M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           S-hydroxynitrilase; chiral synthesis; aliphatic; aromatic; S-cyanohydrin; recombinant; ss.
                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT36351
                                                                                                                                                             Sequence 817 BP; 250 A; 159 C; 193 G; 215 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                         116 CTCCTTGAGGCACTTGGCCACAAGGTTACTGCACTGGACCTTGCA 160
                                                                                                                                                                                                                                                                                                                                           Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hayn EM, Kohlwein S,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /*tag= a
/product= S-hydroxynitrilase
                                                                                                                                                                                                                   Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hevea brasiliensis S-hydroxynitrilase cDNA.
                                                                                                                                                                                                                                                                                                                 to: 817
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Location/Qualifiers
                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: AAT86824 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
                                                                                                                                                                                                                                                                                                                                                                                                                               seq_documentation_block:
ID AAT36351 standard; cDNA; 1091
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       95AT-0001182
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-OCT-1997 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Griengl H, Hasslacher M,
                                                                                                                                                                                                                45.00
3.750
80.000
                                                                                                                                                                                                                                                                                       US-09-485-529-104 x AAT86824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ...830
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         WPI; 1997-119058/11.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hevea brasiliensis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        P-PSDB; AAW10593
                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                   Quality:
                                                                                                                                                                                                                                  Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO9703204-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            10-JUL-1996;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-JUL-1995;
                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 30-JAN-1997
                                                                                                                                                                                                                                                                        alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Schwab H;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAT36351;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Hevea
                                                                                                                                                                                                                                                                                                                                                                                                                                              888888888888888
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than the native enzyme.

H. brasiliensis leaves were homogenised in cold pH 6.5 K phosphate buffer, and the extract subjected to sequential chromatography on OAB-Sepharose, Phenyl-Sepharose and BioGel 150 to recover a protein with a specific activity of 19 IU/mg.

A CDNA library was prepared from young H. brasiliensis leaves in Zap phage, and screened with polyclonal rabbit antiserum raised against the purified enzyme. The insert in one positive clone was isolated, and ligated into pBluescript to form pHNL-100. This plasmid, in E. coli SOLK, expressed a fusion protein with lacz that was immunoreactive. Sequencing showed that the insert in this plasmid was not complete, and the missing 5'-end generated by 2 stage PCR, resulting in plasmid pHNL-101, containing the entire
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /*tag= a
/product= "Keratan sulphate 6-sulphotransferase"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        chick chondroitin 6-sulphotransferase; C6ST; phage Lambda; expression vector; C0S-7 cells; Bluescript plasmid; galactose; keratan sulphate; chondroitin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              KSGal6ST; keratan sulphate 6-sulphotransferase; hybridization;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Keratan sulphate 6-sulpho-transferase polypeptide - transfers sulphate from sulphate donor to galactose 6-hydroxy group etc.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAV36418
                                                                                                                                                                                                                                                                                              Sequence 1091 BP; 326 A; 196 C; 239 G; 330 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          129 CTCCTTGAGGCACTTGGCCACAAGGTTACTGCACTGGACCTTGCA 173
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                      Length: 15
Gaps: 0
Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 1091
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Keratan sulphate 6-sulphotransferase.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
ID AAV36418 standard; cDNA; 1458 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       (SEGK ) SEIKAGAKU KOGYO CO LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              97EP-0309564.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    96JP-0320535
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   14-SEP-1998 (first entry)
                                                                                                                                                                                                                                                                                                                                                                        45.00 · 3.750 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x AAT36351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: AAT36351
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1..1236
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Fukuta M, Habuchi O;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 1998-288750/26.
P-PSDB; AAW61100.
                                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                           coding sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              27-NOV-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    29-NOV-1996;
                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   EP845533-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-JUN-1998
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAV36418;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Key
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Dreier H;

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This nucleic acid sequence is a cDNA coding for human KSGal6ST (Keratan sulphate 6-sulphotransferaes). The sequence was obtained by radiolabelling the cDNA of chick chondroitin 6-sulphotransferaes (C6ST) and using this as a probe in a random oligonucleotide-primed labelling method. Human foetal brain cDNA was inserted into a phage Lambda gill cloning vector whereby the clones containing the KSGal6ST were obtained by hybridization using the prepared probe. The positive clones were subcloned into a recombinant expression vector and used to transform (C6ST) calls, from which calls expressing KSGal6ST can be selected. The phage cDNA inserts were isolated and subcloned into a Bluescript plasmid. Deletion clones were then prepared from which both strands were sequenced betton clones method. The KSGal6ST can which both strands were sequenced sulphate from a sulphate donor to galactose 6-0H groups in keratan sulphate, but does not transfer sulphate to chondroitin, chondroitin
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Porcine reproductive and respiratory syndrome; PRRS; pig; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /note- "especially preferred attenuation site (codon for Tyr-946)"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Porcine reproductive and respiratory syndrome virus ORF1b.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH26333
                                                                                                                                                                                                                                                                                                                            Sequence 1458 BP; 254 A; 526 C; 421 G; 257 T; 0 other;
                                                                                                                                                                                                                                                                                            sulphate A or C, dermatan sulphate or CDSNS heparin.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  syndrome virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /*tag= a
/note= "preferred attenuation site"
2336..2838
/*tag= b
                                                                                                                                                                                                                                                                                                                                                                                                Length: 14
Gaps: 0
Percent Identity: 57.143
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (BOEH ) BOEHRINGER INGELHEIM VETMEDICA GMBH.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: AAV36418 from: 1 to: 1458
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Porcine reproductive and respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             therapy; infection; attenuation; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Location/Qualifiers
2806..2868
                 Claim 9; Page 15-16; 21pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              44.00
3.667
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-485-529-104 x AAV36418
                                                                                                                                                                                                                                                                                                                                                                                                                Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
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The present sequence is that of open reading frame (ORF) 1b of porcine reproductive and respiratory syndrome (PRRS) virus strain ATCC VR-2332. It encodes a 1457 annio acid viral protein (see AAB82665). The invention provides live attenuated PRRS viruses which are attenuated by at least 1 amino acid mutation in a specific site of the viral protein coded by ORF 1b or ORF 2. A claimed live attenuated PRRS virus has at 1 east 1 of the amino acids in positions 321-341 of the ORF1a-encoded protein (see AAB8265), and/or at least 1 of the amino acids in positions 321-341 of the amino acids in positions 1-20 of the ORF 2-encoded protein (see AAB82667) deleted. Of the ORF 1b-encoded protein, and/or at least 1 of the amino acids in positions 1-20 of the ORF 2-encoded protein (see AAB82667) deleted. Other claimed live attenuated PRRS viruses have amino acid 31 of ORF2 deleted or replaced by an amino acid not identical to that of ARCC VR-2332. Specific mutations are created using molecular claimed. The live attenuated PRRS viruses are used in the manufacture of a vaccine for the prophylaxis and treatment of PRRS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Porcine reproductive and respiratory syndrome virus; PRRSV; vaccine; plg; attenuated virus; \ensuremath{\text{ds}} .
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               viruses that are less
                                                                                                                     of.
                                                                                                  Novel live porcine reproductive and respiratory syndrome virus attenuated by mutations in specific site of viral protein coded specified open reading frames, useful for prophylaxis/treatment
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1690 GACAGGATCCTCGCGGCCCTCGCCTATCACATGAAGGCGAGTAATGTTTC 1739
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Seguence 4374 BP; 1026 A; 1197 C; 1109 G; 1042 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC81763
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Porcine Lelystad virus MSV JA-142 attenuated version.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               infections in pigs. Infectious clones of PRRS virus virulent than VR-2332 can be recombinantly produced.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Length: 17
Gaps: 0
Percent Identity: 47.059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: AAH26333 from: 1 to: 4374
                                                                                                                                                                                                   Disclosure; Fig 5a-c; 34pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
ID AAC81763 standard; DNA; 15424 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x AAH26333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      44.00
2.750
94.118
Pesch S,
                                     WPI; 2001-483237/52.
P-PSDB; AABB2666.
                                                                                                                                                             viral infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Lelystad virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              WO200065032-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      02-NOV-2000.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1740 T 1740
Elbers K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       17 a 17
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99US-0461879
                                                                                                                                                                                                                                                                                                                                   Percent Similarity:
                                                                                                                                                                                                                                                                                                                           Ratio:
                                                                                                                                                                                                                                                                                                                Quality:
                     (USDA ) US SEC
                                         Mengeling WL,
15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             12-SEP-2000
                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             9440 T 9440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         AAA27809;
                                                                                                                                                                                                                                                                                                                                                                                                                                                         17 a 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  North
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CDNA.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Key
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The present invention provides a novel method of producing attenuated versions of viruses, using multiple passage through cell cultures and involving the removal of samples of the virus prior to the induction of cytopathic effects. The sample is then inoculated into the next cell culture. The sequence of the naturally-occurring Lelystad virus (also known as the porcine reproductive and respiratory syndrome virus or PRRSV) atypical strain JA-142 is provided, along with that of a modified version of the virus. The modified version can be used in the vaccination of pigs against the Lelystad virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                reproductive and respiratory syndrome virus; PRRSV; vaccine; pig;
                                                                                    Gorcyca DE;
                                                                                                                           Passaging viruses to attenuation comprises maintaining virus in logarithmic phase of replication throughout multiple cell culture passages, useful for protection against atypical porcine reproductive and respiratory syndrome virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sequence 15424 BP; 3380 A; 4083 C; 4008 G; 3953 T; 0 other;
                                                                                    Burkhart K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAC81764
                                                                                                                                                                                                                                                                                                                                                                              Percent Identity: 47.059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Porcine Lelystad virus JA-142 virulent version.
                                                                                   Roof M,
                                                                                                                                                                                                                                                                                                                                                                      Gaps:
                                                                                                                                                                                                                                                                                                                                                           Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 15424
                                                                                                                                                                                Example 7; Page 56-61; 70pp; English.
                                                                                   Lager K,
                                                                                                                                                                                                                                                                                                                                                                                                                                   to: AAC81763 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
ID AAC81764 standard; DNA; 15424
        21-APR-2000; 2000WO-US10852.
                             99US-0298110.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               21-APR-2000; 2000WO-US10852
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     99US-0298110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                                                  Vorwald A,
                                                                                                                                                                                                                                                                                                                                                        44.00
2.750
94.118
                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x AAC81763
                                                            (USDA ) US SEC OF AGRIC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            attenuated virus; ds
                                                                                                       WPI; 2000-687328/67
                                                                                                                                                                                                                                                                                                                                                          Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     WO200065032-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Lelystad virus
                                                                                  Mengeling WL,
                             22-APR-1999;
15-DEC-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      23-FEB-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     22-APR-1999;
                                                                                                                                                                                                                                                                                                                                              alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       9440 T 9440
                                                                                                                                                                                                                                                                                                                                                                                                                                   Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AAC81764;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   17 a 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Porcine
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The present invention provides a novel method of producing attenuated versions of viruses, using multiple passage through cell cultures and involving the removal of samples of the virus prior to the induction of cytopathic effects. The sample is then inoculated into the next cell culture. The sequence of the naturally-occurring Lelystad virus (also known as the porcine reproductive and respiratory syndrome virus or PRRSV) atypical strain JA-142 is provided, along with that of a modified version of the virus. The modified version can be used in the vaccination
                                                        Gorcyca DE;
                                                                                                                                                                        Passaging viruses to attenuation comprises maintaining virus in logarithmic phase of replication throughout multiple cell culture passages, useful for protection against atypical porcine reproductive and respiratory syndrome virus -
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             syndrome virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              North American porcine reproductive and respiratory syndrome virus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      North American PRRS virus; Nidovirales virus; pig; swine; vaccine;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /*tag= b
/*tag= b
/note= "ORFb, encodes polyprotein comprising
replicase (RNA polymerase) and helicase
functions"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /*tag= a
/note= "ORFla, encodes polyprotein comprising
protease function"
7664..12055
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Sequence 15424 BP; 3370 A; 4075 C; 4011 G; 3968 T; 0 other;
                                                        Roof M, Burkhart K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAA27809
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             American porcine reproductive and respiratory
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 17
Gaps: 0
Percent Identity: 47.059
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  to: 15424
                                                                                                                                                                                                                                                                                                                        Example 7; Page 61-66; 70pp; English.
                                                        Lager K,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    of pigs against the Lelystad virus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Location/Qualifiers
192..7685
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               AAA27809 standard; cDNA; 15450
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      (first entry)
                                                        Vorwald A,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
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94.118
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                                                                                                                WPI; 2000-687328/67.
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/note- "ORF2, 12680..13444

/*tag=

encodes small membrane glycoprotein'

"ORF3,

..13761

/note= 13225.. /*tag=

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"ORF5, encodes major envelope glycoprotein"

..14883

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/*tag= h /note= "ORF7, encodes nucleocapsid protein"

Sheppard MG;

98US-0113345 99EP-0309409

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(PFIZ ) PFIZER PROD INC
                                                 Calvert JG, Welch SW,
                                                     WPI; 2000-444364/39.
                                 EP1018557-A2
                                       25-NOV-1999;
                                           22-DEC-1998;
                                    12-JUL-2000
               CDS
                    CDS
                          CDS
     CDS
          CDS
CDS
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The present sequence is that of cDNA corresponding to the North American porcine reproductive and respiratory syndrome (PRRS) virus isolate P129A RNA genome. The cDNA in plasmid p77129A is deposited as ATCC 20348B. The P129 virus was originally isolated from a struct solated repeated from a severe PRRS outbreak, and plaque purified virus P129A was obtained after 10 serial passages from the pig. The DNA sequence includes 8 oper reading frames (ORRS 1a, 1b, 2-7) encoding polyproteins comprising protease, replicase and helicase functions, small membrane pycoproteins, a major envelope crocein, an integral membrane protein and a nucleocapsid protein. The invention provides isolated polynucleotide molecules, plasmids, viral vectors and transfected host cells that comprise plasmids, viral vectors and transfected host cells that comprise molecules, viral vectors and transfected host cells encoding genetically modified North American PRRS viruses that are disabled in their ability to cause PRRS. The invention also provides comprises comprise and other animals. Vaccines comprises and other animals. Vaccines may also comprise a genetically modified North American PRRS viruses that are disabled and North American PRRS viruses that are disabled and North American PRRS viruses, viral vectors and enthods of using these a genetically modified North American PRRS virus comprises and particular personal comprises. New polynucleotide encoding an infectious RNA molecule of a North American porcine reproductive and respiratory syndrome virus for use as a vaccine in protecting swine and other animals from infection by a more heterologous antigenic epitopes, or a plasmid encoding such a PRRS virus. Also provided are isolated polynucleotide molecules, viral vectors, and transfected host cells that comprise a nucleotide sequence encoding a peptide of a North American PRRS virus. These are useful in providing peptides to compensate for mutated peptide coding sequences of DNA sequences encoding genetically modified North American PRRS viruses so that functional virions can be Claim 1; Page 24-29; 53pp; English. pathogen

Sequence 15450 BP; 3398 A; 4060 C; 4041 G; 3951 T; 0 other;

generated

Sequence 29 BP; 5 A; 5 C; 11 G; 8 T; 0 other;

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Aestivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by the treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin insensitive. Taller plants may be made by knocking out Rht or the relevant homologous gene in the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis inhibitor to keep weeds dwarf but let crop plants grow tall. Primers AAX36234-X36254 were used in the course of the invention.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis; paclobutrazol; D8 gene; maize; sequencing primer; ss.
                                                                                                                                                                                           1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                 seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36248
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Primer used for sequencing of the maize D8 gene clones.
           Length: 17
Gaps: 0
Percent Identity: 47.059
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                                                                                                                                      from: 1
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                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
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to
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22.11-10-09-02-02-02-02-02-02-02-02-02-02-02-02-02-	000000000000000000000000000000000000000

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(ASTR ) ASTRA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          This sequence encodes a H. pylori inner membrane protein.

The protein may be used in a vaccine to prevent or treat H. pylori infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors.

The genomic sequence of H. pylori (ATCC 55679) was determined from overlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ONF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ONF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide
                                                                                                                                                                                                                                                                                                           Cytoplasmic; vaccine; prevention; treatment; infection; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis; diagnosis; envelope; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori infection, and to detect Helicobacter
                                                                                                                                                                        seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT67756
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/transl_except= (pos: 871..873, aa: Xaa)
/note= "Xaa = unknown"
                                                                                                                                        105 CTTCTCGAGGCTTTGGGCCATCGTGTAACCGCCTTAGACCTAGGT 149
                                                                                                                        3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
           15
                                   Percent Identity: 60.000
                                                                                                                                                                                                                                                                                    H. pylori inner membrane protein ORF 23493756.aa.
           Length:
                         Gaps:
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                                                                                                  from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Claim 1; Page -; 1481pp; English.
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80.000
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                                                                                                                                                                                                                                                                                                                                                                                                  ..897
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P-PSDB; AAW20252.
                                                                                                                                                                                                                                                                                                                                                             Helicobacter pylori.
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                         Ratio:
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                                                                                                  Align seg 1/1
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Helicobacter pylori has been strongly linked to chronic gastritis and duodenal ulcer disease. The nucleic acid sequences of the invention are used to evaluate compounds, especially activators or inhibitors of bacterial life cycle, for the ability to bind an H. pylori nucleic acid sequence. The nucleic acid sequences, and corresponding proteins, are also useful for generating vaccines for immunising subjects against H.
production, e.g. in E. coli hosts.
Note: This DNA sequence is not reproduced in the specification and has
been derived from the related specification, WO9719098.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Transmembrane; cytoplasmic; cell envelope; flagella; transport; secreted; periplasmic; chronic gastritis; duodenal ulcer disease; activator; inhibitor; bacterial life cycle; vaccine; immunise; detection; antisense; inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Helicobacter pylori nucleic acid sequences and related proteins used for diagnostics and therapeutics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 aa: Xaa)
aa: Xaa)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT77436
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                                                                                                                          Sequence 894 BP; 316 A; 150 C; 170 G; 256 T; 2 other;
                                                                                                                                                                                                                                                 Length: 16
Gaps: 0
Percent Identity: 37.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              BP
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        pylori or for use in detecting the presence of Helicobacter species in a sample. Antisense nucleic acid sequences of these sequences are used to inhibit expression of a gene from Helicobacter species. H. pylori whole genomic DNA was isolated and nebulised to a median size of 2000 bp. Purified DNA fragments were blunt-ended and ligated to unique batxII-linker adapters in 100-1000 fold molar excess. These linkers are complementary to the BstXI-cut pMPX vectors, while the overhang is not self-complementary. Therefore the linkers will not concatemerise nor will the cut vector re-ligate itself easily. The linker-adapter inserts shotgun subclone libraries. The purified DNA samples were then
                                                                                                                                                                       Note: The ORF/protein reference number for this sequence was obtained from the related specification, WO9640893.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Hybridisation assay; genetic mapping; gene expression control; protein identification; signal transduction pathway; metabolic pathway; promoter; termination sequence; ss.
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                                                                                                                                                                                                                   Sequence 894 BP; 316 A; 150 C; 170 G; 256 T; 2 other
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Gaps: 0
Percent Identity: 37.500
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XX
AC47916 standard; DNA; 1325 BP.
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AC47916;
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AC47916;
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AAC47916;
XX
Bridgesis thaliana DNA fragment
XX
Hybridisation assay; genetic mappi
protein identification; signal tra
XX
Arabidopsis thaliana.
XX
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C3-WAR-1999; 99US-012874.
PR
C3-APR-1999; 99US-013874.
PR
C3-APR-1999; 99US-013874.
PR
C3-APR-1999; 99US-013874.
PR
C3-APR-1999; 99US-013874.
PR
C3-APR-1999; 99US-013049.
PR
C3-APR-1999; 99US-0131449.
PR
C3-APR-1999; 99US-0131449.
PR
C3-APR-1999; 99US-0131449.
PR
C3-APR-1999; 99US-0132407.
                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-485-529-104 x AAT77436/rev
                                                                                                                                                                                                                                                                     42.00
2.800
93.750
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Percent Similarity:
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Recombinant or substantially pure preparations of H. pylori polypeptides are disclosed, together with the nucleic acids encoding them. In all, 73 ORFs are shown. The proteins are variously cell envelope proteins,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Helicobacter pylori nucleic acids and proteins - used to develop products for the detection, prevention and treatment of H. pylori infections
                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAX30475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               H. pylori secreted protein ORF hp6p10606_23493756_c1_21
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Vaccine; probe; diagnostic; ORF; cell envelope protein; secreted protein; cellular protein; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Identity: 60.000
                                                                                                                                                                                                                                                                          Length:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
ID AAX30475 standard; DNA; 1464 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             97US-0891928.
96US-0739150.
96US-0759739.
              990S-0160814.
990S-0160815.
990S-0160815.
990S-0160980.
990S-0161404.
990S-0161406.
990S-0161359.
990S-0161360.
990S-0161369.
990S-0161369.
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 99US-0160770
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P-PSDB; AAY11008.
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Ratio:
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28-OCT-1996;
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21-0CT-1999;
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22-0CT-1999;
22-0CT-1999;
22-0CT-1999;
25-0CT-1999;
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28-0CT-1999;
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28-0CT-1999;
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990S-0157865.
990S-0158029.
990S-0158232.
990S-0159293.
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99US-0156596.
99US-0157117.
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99US-0159329.
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99US-0159331.
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99US-0160767.
99US-0160768.
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99US-0159638.
99US-0159584.
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08-057-1999

13-057-1999

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              22 - JUL - 1999
23 - JUL - 1999
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23 - JUL - 1999
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04 - AUG - 1999
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09-AUG-1999;
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10-AUG-1999;
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21-OCT-1999;
21-OCT-1999;
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18-AUG-1999;
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06-OCT-1999;
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16-AUG-1999
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23-AUG-1999
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secreted proteins or other cellular proteins. Vaccines containing the nucleic acids or proteins are claimed, as are probes containing at least 8 nucleotides from the nucleic acid sequences. The vaccines are useful for treating or reducing the risk of H. pylori infections, and the probes can be used diagnostically for detecting the presence of Helicobacter in a sample. The products are also of use in screening for compounds having the ability to interfere with the H. pylori life cycle or to inhibit H. pylori infection.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Cytoplasmic; vaccine; prevention; treatment; infection; envelope; identification; binding compound; bacterium; life cycle; activator; bacteria; inhibitor; duodenal ulcer disease; chronic gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Helicobacter pylori nucleic acid sequences and related polypeptide(s) - useful for vaccines to treat or prevent H. pylori
                                                                                                                                                                                                                                                                                                                                                                611 GAGATTTTAACATCATTAGGATTTAGGATAAGAATGTCTAATTTGTCT 564
                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1997.DAT:AAT68140
                                                                                                                                                                                                                                                                                                                                            2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                          Sequence 1464 BP; 545 A; 273 C; 276 G; 370 T; 0 other;
                                                                                                                                                                                                                                                                                                                   to: 1464
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    pylori inner membrane protein ORF 13ep12003orf20.
                                                                                                                                                                                                       Length: 16
Gaps: 0
Percent Identity: 37.500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1..1554
/*tag= a
/note= "no stop codon given"
                                                                                                                                                                                                                                                                                                                 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Mellgaerd BL;
                                                                                                                                                                                                                                                                                                               to reverse of: AAX30475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Claim 1; Page 924; 1481pp; English
                                                                                                                                                                                                                                                                                  US-09-485-529-104 x AAX30475/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                        AAT68140 standard; DNA; 1554
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                96US-0630405.
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                                                                                                                                                                                                     42.00
2.800
93.750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Helicobacter pylori.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          WPI; 1997-052306/05.
P-PSDB; AAW20887.
                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
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                                                                                                                                                                                                       Quality:
Ratio:
                                                                                                                                                                                                                                    Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (ASTR ) ASTRA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               diagnosis; ds
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   06-JUN-1996;
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                                                                                                                                                                                        alignment_scores
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                                                                                                                                                                                                                                                                                                               Align seg 1/1
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infection or to identify H. pylori polypeptide binding compounds, useful as potential H. pylori life cycle activators or inhibitors. The genomic sequence of H. pylori (ATCC 55/59) was determined from coverlapping contigs generated by mechanically shearing the bacterial DNA. The sequences were analysed for ORF of at least 180 nucleotides, and the predicted coding regions defined by computer evaluation. To identify likely H. pylori antigens for vaccine development, the amino acid sequences predicted from various ORF were analysed for significant homology to other known or exported membrane proteins. Having identified and determined the sequences of interest, particular regions can be isolated from H. pylori by PCR amplification for recombinant polypeptide production, e.g. in E. coli hosts.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 protein; Helicobacter infection; gastroduodenal disease; gastritis;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          develop products
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        New isolated Helicobacter polynucleotides - used to develop
for the diagnosis, prevention and treatment of Helicobacter
infections and gastrointestinal diseases
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Tomb J;
                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1998.DAT:AAX14024
                                                                                                                                                                                                                                                                                                                                                                                                              2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                       Sequence 1554 BP; 571 A; 281 C; 290 G; 412 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                 to: 1554
                                                                                                                                                                                                                                                                   Length: 16
Gaps: 0
Percent Identity: 37.500
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
51..1514
/*tag= a
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97US-0833457.
97US-0881227.
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ID AAX14024 standard; DNA; 1564
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US-09-485-529-104 x AAT68140/rev
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 peptic ulcer disease; ss.
                                                                                                                                                                                                                                                                   42.00
2.800
93.750
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  H. pylori GHPO 479
                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          W09843478-A1
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                                                                                                                                                                                                                                                      alignment_scores:
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24-JUN-1997;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Key
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Claim 1; Page 391-394; 2054pp; English.

This sequence encodes a H. pylori inner membrane protein. The protein may be used in a vaccine to prevent or treat H. pylori

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This sequence represents a polynucleotide of the invention. It was isolated from Helicobacter pylori and encodes a H.pylori GHPO protein. The polypeptides can be used for preventing or treating Helicobacter infections, and gastroducdenal diseases associated with these infections, including acute, chronic, and atrophic gastritis, and peptic ulcar diseases, e.g. gastric and duodenal ulcers. They can also be used for the production of antibodies. The products can also be used for detection and diagnosis.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           and its flanking regions was determined (AAQ66797). The spheroidin gene can be used as the location for insertion of heterologous DNA in insect and mammalian expression systems. A spheroidin-like gene was also identified in CDEPV and its amino acid sequence was
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 New entomopoxvirus polynucleotide sequences, proteins and vectors - are used for expression of heterologous proteins in both insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of the Amsacta moorel entomopoxvirus spheroidin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Spheroidin; gene expression; vector; insect cell culture;
                                                                                                                                                                                                                                                                                                                                                                                                                                                  661 GAGATTTTAACATCACTAGGGTTTAGGATAAGAATGTCTAATTTGTCT 614
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ66825
                                                                                                                                                                                                                                                                                                                                                                                                               2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                             Sequence 1564 BP; 576 A; 285 C; 294 G; 409 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: AAX14024 from: 1 to: 1564
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Choristoneura biennis entomopoxvirus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Disclosure; Page 87; 118pp; English
                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-485-529-104 x AAX14024/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAQ66825 standard; DNA; 235
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CbEPV spheroidin gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-217887/26
                                                                                                                                                                                                                                                                                    Percent Similarity:
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*0000000000x8
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ВР

culture; AmEPV; CbEPV; Amsacta moorei;

Moyer RW

Hall RL,

92US-0991867 93WO-US11907

Laugin: 16 Gaps: 0 Percent Identity: 37.500

42.00 2.800 93.750

Quality:

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and its flanking regions was determined (AAQ66797). The spheroidin gene can be used as the location for insertion of heterologous DNA in insect and mammalian expression systems. A spheroidin-like gene was also identified in CfEPV and its amino acid sequence was deduced (AAR55587).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          New entomopoxvirus polynucleotide sequences, proteins and vectors - are used for expression of heterologous proteins in both insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            The sequence of the Amsacta moorei entomopoxvirus spheroidin gene
                                                                                                                                                                                                                                                                                                                                               Spheroidin; gene expression; vector; insect cell culture; mammal cell culture; AmEPV; CfEPV; Amsacta moore1;
                                                                                                                                                                                         seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ66826
           Length: 14
Gaps: 0
Percent Identity: 64.286
                                                                                                                                                    Percent Identity: 64.286
                                                                                                                                    2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           73 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Length:
                                                                                                                                                                                                                                                                                                                                                                                                      Choristoneura fumiferana entomopoxvirus.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ::
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Align seg 1/1 to: AAQ66826 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Sequence 235 BP; 95 A; 25 C; 42
                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     93WO-US11907.
                                                                                                                                                                                                                      seq_documentation_block:
ID AAQ66826 standard; DNA; 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92US-0991867.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Moyer
                                                                                                                                                                                                                                                                                          (first entry)
           41.00
3.727
78.571
                                                                             US-09-485-529-104 x AAQ66825
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 41.00
3.727
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US-09-485-529-104 x AAQ66826
                                                                                                          Align seg 1/1 to: AAQ66825
                                                                                                                                                                                                                                                                                                                    CfEPV spheroidin gene.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gruidl ME, Hall RL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            (UYFL ) UNIV FLORIDA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1994-217887/26.
                                                                                                                                                                                                                                                                                                                                                                         entomopoxvirus; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
                        Ratio:
Percent Similarity:
              Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-DEC-1993;
                                                                                                                                                                                                                                                                                          18-JAN-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-DEC-1992;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                WO9413812-A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                           23-JUN-1994
                                                                   aliqnment_block
                                                                                                                                                                                                                                                               AAQ66826;
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2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15

Seguence 235 BP; 96 A; 20 C; 42 G; 77 T; 0 other;

Choristoneura fumiferana entomopoxvirus spheroidin-like gene sequence

(first entry)

28-OCT-1999

AAZ10093;

seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ10093 2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15

BP

seq_documentation_block: ID AA210093 standard; DNA; 235

; to

from: 1

AAZ10092

to:

Align seg 1/1

US-09-485-529-104 x AAZ10092

Spheroidin; Entomopoxvirus; expression system; replication; heterologous gene expression; thymidine kinase; poxvirus; vaccinia; swinepox virus; insect pest control; immunity; ss.

Choristoneura fumiferana entomopoxvirus

US5935777-A.

10-AUG-1999

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The sequence. It is used to make the expression systems of the invention. The specification describes an EPV expression system that is capable of directing the replication and expression of a heterologous gene in a selected host cell. The expression system comprises an EPV promoter sequence operably linked to the selected heterologous gene in a selected host cell. The expression of selected heterologous gene sequence operably linked to the selected proteins in the expression system is used for the expression of sequence. The expression of selected proteins in insect and mammalian host cells e.g. human, rodent and primate cells. EPV thymidine kinase and spheroidin genes can also be used in vertebrate poxylivuses such as vaccinia and swinepox virus. The expression vectors can also be used for the control of insect pests through the insertion of a gene encoding an insect toxin into the expression vector which will infect the target pest and produce large quantities of the toxin. Spheroidin and thymidine kinase are nonessential chert are capable of operating in a vertebrate poxylivus (e.g. vaccinia) they are capable of operating in a vertebrate poxylivus (e.g. vaccinia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             present sequence represents an Entomopoxvirus (EPV) spheroidin-like
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Novel expression system for the expression of heterologous sequences in insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Spheroidin; Entomopoxvirus; expression system; replication; heterologous gene expression; thymidine kinase; poxvirus; vaccinia; swinepox virus; insect pest control; immunity; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                            Choristoneura biennis entomopoxvirus spheroidin-like gene sequence.
                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAZ10092
stimulate cell-mediated and humoral immunity
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Example 10; Column 99-102; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Moyer RW;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Choristoneura biennis entomopoxvirus.
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                                                                                                                                                                                     seq_documentation_block:
ID AAZ10092 standard; DNA; 235 BP.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            95US-0544332.
91US-0657584.
92US-0827685.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        95US-0544332
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                92US-0991867
                                                                                                                                                                                                                                                                                                                                                                    (first entry)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                WPI; 1999-457596/38.
P-PSDB; AAY30179.
                                                                                                                                                                                                                                                                                                                                                                    28-OCT-1999
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (UYFL ) UNIV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        17-OCT-1995;
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07-DEC-1992;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            17-0CT-1995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              19-FEB-1991
30-JAN-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gruidl ME,
                                                                                                                                                                                                                                                                                                AAZ10092;
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Sequence 235 BP; 96 A; 20 C; 42 G; 77 T; 0 other;
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The present sequence represents an Entomopoxvirus (EPV) spheroidin-like gene sequence. It is used to make the expression systems of the invention. The specification describes an EPV expression system that is capable of directing the replication and expression of a heterologous gene in a selected host cell. The expression system comprises an EPV promoter sequence operably linked to the selected heterologous gene sequence operably linked to the selected heterologous gene promoter sequence operably linked to the selected proteins in heterologous sequences and the production of selected proteins in the the thymidine kinase and spheroidin genes can also be used in vertebrate poxviruses such as vaccinia and swinepox virus. The expression vectors can also be used for the control of insect pests through the insertion of a gene encoding an insect toxin into the expression vector scan also be used for the control of insect pests through the insertion of a gene encoding an insect toxin into the capterial protein which which will infect the target pest and produce large quantities of the toxin. Spheroidin and thymidine kinase are nonessential proteins which makes them ideal for the insertion of exogenous DNA and mammalian coll expression vectors whom we have the provential provider sequences are nonessential provided by the control of insect poxvirus (e.g. vaccinia).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Novel expression system for the expression of heterologous sequences in insect and mammalian host cells
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               mammalian cell expression vector system. Pox viruses are able to
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      immunity.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Example 10; Column 101-102; 72pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        stimulate cell-mediated and humoral
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Moyer RW;

Li Y,

Hall RL,

Gruidl ME,

WPI; 1999-457596/38 P-PSDB; AAY30180

(UYFL ) UNIV FLORIDA RES FOUND INC.

92US-0991867

95US-0544332. 91US-0657584. 92US-0827685. 92WO-US00855.

30-JAN-1992 12-FEB-1992

07-DEC-1992

95US-0544332,

17-0CT-1995;

17-0CT-1995 .9-FEB-1991 Sequence 235 BP; 95 A; 25 C; 42 G; 73 T; 0 other;

Length: 14 Gaps: 0 Percent Identity: 64.286

41.00 3.727 78.571

Ratio:

Quality:

alignment_scores:

Percent Similarity:

alignment_block:

alignment_scores:

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The specification describes polypeptides encoded by the Rht gene (and its homologues) that, when expressed in Triticum Asstivum, inhibit growth of the plant. This growth inhibition is antagonised by gibberellin. The products can be used to provide Rht expression in plants, conferring a dwarf phenotype on a plant which is correctable by treatment with gibberellin. In addition, the products can be used to produce Rht mutant plants which are dwarfed compared with wild-type, the dwarfing being gibberellin-insensitive. Taller plants may be made which are resistant to the plant of interest. Plants may be made which are resistant to compounds which inhibit gibberellin biosynthesis, such as paclobutrazol, e.g. to allow use of a gibberellin biosynthesis such as paclobutrazol, dwarf but let crop plants grow tall. The present sequence was dwarf but let repartially sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              New Triticum Aestivum polynucleotides - encode a polypeptide which provides inhibition of the growth of plants, which inhibition is antagonised by gibberellin, used to confer a dwarf phenotype
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Rht gene; homologue; Triticum aestivum; wheat; growth inhibition; antagonist; gibberellin; dwarf phenotype; gibberellin biosynthesis;
                                                                                                                                                                                                                                                                                                                                                                                                                                 DNA sequence obtained after sequencing wheat Rht clone 5al.
                                                                                                                                                                                                                                                       seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1999.DAT:AAX36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 285 BP; 39 A; 89 C; 100 G; 46 T; 11 other;
                                      Percent Identity: 64.286
                                                                                                                                                                                                                  84 GAATTATTGAACGTCAAAGGTTATCCTGTTAAAGCATCCGAT 125
                                                                                                                                                                          2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
Length:
                                                                                                                                   Align seg 1/1 to: AAZ10093 from: 1 to: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Disclosure; Fig 2c(4); 88pp; English.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Harberd NP, Peng J, Richards DE;
                                                                                                                                                                                                                                                                                                               AAX36271 standard; DNA; 285 BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BIOSCIENCE LTD.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    98WO-GB02383.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        97GB-0017192.
                                                                                                                                                                                                                                                                                                                                                                                            16-JUL-1999 (first entry)
41.00
3.727
78.571
                                                                                               US-09-485-529-104 x AAZ10093
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           WPI; 1999-181040/15.
                                                                                                                                                                                                                                                                                             seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              paclobutrazol; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Triticum aestivum
                                    Percent Similarity:
  Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 (PLAN-) PLANT
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          13-AUG-1997;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9909174-A1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    07-AUG-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             25-FEB-1999
                                                                            alignment block;
                                                                                                                                                                                                                                                                                                                                                      AAX36271;
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Gaps: 0 Percent Identity: 88.889

5.125 88.889

41.00

Quality: Ratio:

alignment_scores:

Percent Similarity:

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Human; cancer; ulcer; HIV infection; human immunodeficiency virus;

W antiinflammatory; antirheumatic; antiarthritic; immunosuppressive;

W antibacterial; endocrine; cardiant; central nervous system; virucide;

W anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; anaemia;

Antiaggregant; haemostatic; vulnerary; antiuloer; osteopathic; eczema;

W dermatological; antiallergic; antiasthmatic; antidiabetic; cytostatic;

W neuroprotective; antidepressant; nootropic; antiparkinsonian; infection;

Immunostimulant; gene therapy; antisense therapy; vaccine; inflammation;

M neurophylactic; rheumatod arthritis; septic shock; pancreatitis;

M cardiac dysfunction; neuropathology; cardiac anaphylaxis; autoimmunity;

W genetic disease; haematopoletic disorder; platelet disorder; asthma;

thrombocytopaenia; osteoporosis; severe combined immunodeficiency;

M allergic rhinitis; diabetes; multiple sclerosis; depression;

M Alzabainer's disease; Parkinson's disease; neurodegenerative disorder;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AAM25966 to AAM99904 encode the human proteins given in AAM2525 to AAM25963. The proteins can have activities based on the tissues and calls they are expressed in, such as: antiinflammatory; antirheumatic; antiarthritic; immunosuppressive; antibacterial; endocrine; cardiant; central nervous system, virucide; anti-HIV; fungicide; antimutagen; cardiovascular; antianaemic; antiaggregant; haemostatic; vulnerary; antiulcer; osteopathic; dermatological; antialergic; antiasthmatic; antiparkinsonian; and immunostimulant. The proteins and polynucleotides encoding them can be used in gene therapy, antisense therapy and vaccine production, The proteins and polynucleotides are useful for screening for agonists or antagonists of a protein and for the treatment and diagnosis of disorders associated with the activity of a protein e.g. inflammation,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Isolated human polynucleotides encoding polypeptides, useful for the treatment and diagnosis of e.g. cancer, ulcers and HIV infection - \,
                                                                                                                                                                                                     seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH99418
                                                               to: 285
                                                                                                                                                                                                                                                                                                                                                                                                          Human protein encoding cDNA sequence SEQ ID NO:253.
                                                               from: 1
                                                               to reverse of: AAX36271
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Claim 1; Page 410; 1217pp; English.
                                                                                                                                                        283 GGGTACAAGGNGCGCGCATCNGACATG 257
                                                                                                           8 GlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                         BP
                                                                                                                                                                                                                                                 seq_documentation_block:
ID AAH99418 standard; cDNA; 556
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          rang YT, Liu C, Drmanac RT;
alignment_block:
US-09-485-529-104 x AAX36271/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               23-DEC-1999; 99US-0471275.
21-JAN-2000; 2000US-0488725.
25-APR-2000; 2000US-0552317.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          22-DEC-2000; 2000WO-US35017
                                                                                                                                                                                                                                                                                                                                                               (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       neurological disorder; ss
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2001-457603/49.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               (HYSE-) HYSEQ INC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              P-PSDB; AAM25477
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Homo sapiens.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             26-JUL-2001.
                                                                                                                                                                                                                                                                                                                                                             16-OCT-2001
                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                   AAH99418;
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Page 35

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The present invention describes a purified or isolated nucleic acid sequence (I) consisting essentially of one of the 93 nucleotide sequences yequence (I) consisting essentially of one of the nucleic acid in a microorganism is capable of inhibiting proliferation of a microorganism. (I) have antibacterial and antibiotic activities, and can be used in gene therapy. Expression of (I) in a microorganism inhibits proliferation of the microorganism on the manufactured antibiotic is useful for reducing the activity or level of a gene product required for proliferation of a microorganism in a subject, specifically humans. The nucleic acids that inhibit bacterial growth or proliferation can be used
rheumatoid arthritis, septic shock, pancreatitis, cardiac dysfunction, neuropathology, cardiac anaphylaxis, viral, bacterial, HIV and fungal infections, autoimmunity, genetic diseases, haematopoietic diseaders, anaemia, platelet disorders, thrombocytopaenia, wounds, burns, ulcers, osteoporosis, severe combined immunodeficiency, eczema, allergic rhintits, asthma, diabetes, cancer, multiple sclerosis, depression, Alzheimer's disease, parkinson's disease, neurodegenerative and neurological disorders.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Escherichia coli protein encoding nucleotide sequence SEQ ID NO:262
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acids encoding proteins required for Escherichia coli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Escherichia coli; identification; proliferation; microorganism; antimicrobial; antibacterial; antibiotic; gene therapy; diagnosis; bacterial growth inhibition; ds.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   proliferation, useful for screening for antimicrobial agents
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAH81463
                                                                                                                                                                                 Sequence 556 BP; 153 A; 125 C; 128 G; 150 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                      556
                                                                                                                                                                                                                                                                                                     Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                294 ATGATGGCAGCATTGGGATACAGTGTGAAAAGCAGCACATTG 253
                                                                                                                                                                                                                                                                                                                                                                                                                                           3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                                                                                                                                                      from: 1
                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Claim 9; Page 393-395; 596pp; English.
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                                                                                                                                                                                                                                                                                                                                                                                                      to reverse of: AAH99418
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   BP
                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-485-529-104 x AAH99418/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   DNA; 1476
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-SEP-2001 (first entry)
                                                                                                                                                                                                                                                         41.00
3.154
92.857
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        (ELIT-) ELITRA PHARM INC
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Forsyth RA, Ohlsen KL,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               _documentation_block:
AAH81463 standard; 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WPI; 2001-457376/49
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                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                Quality:
                                                                                                                                                                                                                                                                                  Ratio:
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                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AAH81463;
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as antisense therapeutics for killing bacteria. In addition to therapeutic applications, the nucleic acid sequences complementary to sequences required for proliferation can be used as diagnostic tools. For example, nucleic acid probes complementary to proliferation-required sequences that are specific for particular species of microorganisms can be used as probes to identify particular microorganism species in clinical specimens. AAMB1295 to AAMB1487 encode the Escherichia coli proteins given in AAG98239 to AAAB41431, and AAH81488 to AAMB1491 represent oligonucleotides, which are used in the exemplification of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine;
antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
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Scalato E, Scarselli
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Neisseria gonorrheae ORF 092 partial DNA sequence SEQ ID NO:309
                                                                                                                                                                                                                                                                                                                                                                             109 GAAGITCTGGCCAATGAAGGITATCAGATCAGTGGTTCCGATTTAGCG 156
                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AAZ53179
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                                                                                                                                                           Sequence 1476 BP; 330 A; 372 C; 436 G; 338 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                   2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla
                                                                                                                                                                                                                  Length: 16
Gaps: 0
Percent Identity: 50.000
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Ratti
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Rappuoli R,
                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: AAH81463 from: 1
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98US-0103796.
99US-0121528.
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81.250
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US-09-485-529-104 x AAH81463
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Venter JC;
                                                                                                                                                                                                                    41.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Neisseria gonorrheae
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                                                                                                                                  present invention.
                                                                                                                                                                                                                    Quality:
Ratio:
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                                                                                                                                                                                                                                               Percent Similarity:
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09-OCT-1998;
25-FEB-1999;
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02-SEP-1998;
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Tettelin H,
                                                                                                                                                                                                        alignment_scores
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P-PSDB; AAY74418
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antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia;
antibacterial; gene therapy; ds.
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Scalato E, Scarselli M;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1521 BP; 359 A; 430 C; 394 G; 338 T; 0 other;
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Gaps: 0
Percent Identity: 56.250
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Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        to: 1521
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   Pizza M, Rappuoli R,
Claim 7; Page 288; 1453pp; English.
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AAZ53180 standard; DNA; 1521 BP.
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98US-009894.
98US-0103749.
98US-0103794.
98US-0103796.
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Ratio: 3.154
Percent Similarity: 81.250
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Venter JC;
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Petersen J,
Tettelin H,
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09-0CT-1998;
09-0CT-1998;
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\overset{\alpha}{\times}\overset{\circ}{\times}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\circ}\overset{\circ}{\c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represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ5457 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as manufacture of medicaments for treating or preventing in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves have use as antibacterial agentis. The polynucleotides of the invention may also be used in gene therapy protocols.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Neisseria meningitidis; Neisseria gonorrheae; antigen; vaccine; antigenic; diagnosis; immunogenic; infection; meningitis; septicaemia; antibacterial; gene therapy; ds.
                                                                                                                                            AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Neisseria meningitidis ORF 092 partial DNA sequence SEQ ID NO:313.
Novel Neisserial polypeptides predicted to be useful antigens for vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2000.DAT:AA253181
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1521 BP; 352 A; 444 C; 396 G; 329 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Identity: 56.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           to: 1521
                                                                                     Claim 7; Page 289; 1453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AAZ53180 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAZ53181 standard; DNA; 1521 BP.
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9805-0094869.
9805-0099894.
9805-0103749.
9805-0103794.
9805-0103796.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         41.00
3.154
81.250
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(GENO-) INST GENOMIC RES.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-09-485-529-104 x AAZ53180
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Neisseria meningitidis
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             31-JUL-1998;
02-SEP-1998;
02-SEP-1998;
09-OCT-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                21-MAR-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WO9957280-A2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              30-APR-1999;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         11-NOV-11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     01-MAY-1998;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       25-FEB-1999;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block
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AAQ71977 is the DNA sequence of murine IL-2R gamma AAR59094, this was used in the development of a claimed method for the diagnosis of X-linked severe combined immunodeficiency (XSCID), in female carriers and male sufferers.
                                                                                                                                   Diagnosis of X-linked severe combined immunodeficiency (XSCID) comprises detecting mutated IL-2R gamma gene, also vectors and transgenic animals containing the mutated gene
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA2001.DAT:AAS06754
                                                                                                                                                                                                                                                                                   Sequence 1608 BP; 413 A; 434 C; 349 G; 412 T; 0 other;
                                                                                                                                                                                                                                                                                                                                    Length: 13
Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 14
                                                                                                                                                                                                                                                                                                                                                                                                                                 to reverse of: AAQ71977 from: 1
                                         (USSH ) US DEPT HEALTH & HUMAN SERVICES
                                                                   Noguchi M;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Manning G,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ВР
                                                                                                                                                                                       Example 1; Fig 7; 98pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAS06754 standard; cDNA; 2730
                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-485-529-104 x AAQ71977/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             22-NOV-2000; 2000WO-US32085.
  93US-0031143.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       99US-0167482
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          (first entry)
                                                                                                                                                                                                                                                                                                                                                    3.727
84.615
                                                                   Leonard WJ, Mcbride WO,
                                                                                                                                                                                                                                                                                                                                       41.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Whyte D,
Clary D;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 WPI; 2001-343950/36.
P-PSDB; AAU03554.
                                                                                              WPI; 1994-303046/37.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                (SUGE-) SUGEN INC.
                                                                                                          P-PSDB; AAR59094
                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                                                                                                                                                                                                                                                                                       Quality:
                                                                                                                                                                                                                                                                                                                                                     Ratio:
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  12-MAR-1993;
14-SEP-1993;
                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        12-SEP-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plowman GD,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   31-MAY-2001
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Flanagan P,
                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAS06754;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Homo
    AAZ53015 to AAZ54536, AAZ54577 to AAZ54615, and AAY74253 to AAY75941 represent novel Neisseria meningitis and N. gonorrheae polynucleotides and polypeptides. AAZ54577 to AAZ54576 and AAZ54616 to AAZ55473 represent PCR primers used in the exemplification of the present invention. The polypeptides, the polynucleotides, antibodies and compositions of the invention can be used as vaccines, as diagnostic reagents, and as immunogenic compositions. The polypeptides can be used in the manufacture of medicaments for treating or preventing infection due to Neisserial bacteria (e.g. meningitis and septicaemia), to detect the presence of Neisseria bacteria, or to raise antibodies. They may also be used to screen for agonists or antagonists, which may themselves may also be used in gene therapy protocols.
                Σ
  Masignani V, Mora M;
Scalato E, Scarselli
                                                                                            Novel Neisserial polypeptides predicted to be useful antigens for
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Murine IL2-R gamma; X-linked severe combined immunodeficiency; XSCID; interleukin; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       181 GAAGTCTTGCACAATTTGGGTTTTAAAGTTTCCGGTTCGGATCAGGCG 228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_name: /SIDS2/gcgdata/geneseq/geneseqn/NA1994.DAT:AAQ71977
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /transl_except= pos:1015..1017, aa:His
25..82
                                                                                                                                                                                                                                                                                                                                                  Sequence 1521 BP; 353 A; 436 C; 397 G; 335 T; 0 other;
                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 56.250
  Hickey E,
Ratti G,
                                                                                                                                                                                                                                                                                                                                                                                                       Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 to: 1521
                                                                                                                                 Claim 7; Page 290-291; 1453pp; English
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Location/Qualifiers
25..1134
 Fraser C, Galeotti C, Grandi G,
Petersen J, Pizza M, Rappuoli R,
Tettelin H, Venter JC;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 25..82
/*tag= b
/note= "Putative"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: AA253181 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
ID AAQ71977 standard; DNA; 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          94WO-US02891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        03-MAY-1995 (first entry)
                                                                                                                                                                                                                                                                                                                                                                                                    41.00
3.154
81.250
                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-485-529-104 x AAZ53181
                                                                                                         vaccines and diagnostics
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Murine IL-2R gamma gene.
                                                    2000-062150/05
                                                                  P-PSDB; AAY74419
                                                                                                                                                                                                                                                                                                                                                                                                     Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                              Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          10-MAR-1994;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Mus musculus
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       WO9420641-A
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                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
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Fraser C,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              AAQ71977;
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to: 1608

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Nucleic acids encoding human kinase polypeptides, useful for preventing
                                                                               Human; protein kinase; PTK; STK; cancer; cardiovascular disease; metabolic disorder; immune related disease; neurological disorder; neurodegenerative disorder; inflammatory disorder; infectious disease; reproductive disorder; gene therapy; ss.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Martinez R;
Polynucleotide sequence encoding human protein kinase #54.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Sudarsanam S,
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diagnosing and/or treating e.g. cancer, immune, cardiovascular and neuronal-associated diseases, and microbial infections -

Example 1; Figure 1; 433pp; English.

AASO6701-AASO6757 encode for novel human protein kinases #1-57. The
novel protein kinases have been identified as members of the tyrosine
or serine/threonine kinase (PTK and STK) families. The polynucleotides
concoing protein kinases and the polypeptides may be used in the
prevention, diagnosis and treatment of diseases associated with
the prevention, diagnosis and treatment of disease associated with
the prevention, diagnosis and treatment of disease associated with
the prevention of an ancers of haematopoletic origin), cardiovascular
cancers (e.g. atherosclerosis), metabolic disorders (e.g. diabetes),
immune related diseases (e.g. rheumatoid arthritis), neurological
disorders (e.g. schizophrenia), neurodegenerative disorders (e.g. asthma), infectious
cdisorders (e.g. HIV) and reproductive disorders (e.g. infertility).
Additionally, polynucleotides encoding protein kinases may be
used for gene therapy and as DNA probes in diagnostic assays.
Che protein kinase polypeptides may be used as antigens in the production
of antibodies against the protein kinases and in assays to identify
modulators of protein kinase expression and activity. 

Sequence 2730 BP; 821 A; 516 C; 602 G; 791 T; 0 other;

41.00 Length: 14 3.154 Gaps: 0 92.857 Percent Identity: 50.000 alignment\_scores:
 Quality:
 Ratio:
 Percent Similarity:

alignment\_block: US-09-485-529-104 x AAS06754/rev

Align seg 1/1 to reverse of: AAS06754 from: 1 to: 2730

3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16

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EST402683 KV1 Medic
EST402683 KV1 Medic
EST3998063 KV0 Medic
NF018F100R1F1000 No
NF059C03ST1F1020 De
NF015E11ST1F1086 De
NF015E11ST1F1080 De
NF075B05ST1F1000 De
NF046C05ST1F1000 De
S NF046C05ST1F1000 De
S NF046C05ST1F1000 De
S EST468300 MHAM Medi
                                                                                                                                                                                                                                                                                                                                                                        A WOO 3835 Cryptomeri
5 AV236965 RIKEN full
2 MU02402.x1 Soares m
3 MU02402.x1 Soares m
4 RPCI-23-467N11.TV R
1 RPCI-23-467N11.TV R
9 BB368429 RIKEN full
3 BB0101992 RIKEN full
2 BB101992 RIKEN full
3 BB101992 RIKEN full
5 BB101992 RIKEN full
                                                                                                                                                           NF003E05STIF1000 De
NF040G10STIF1000 De
NF040G10STIF1000 De
NF064E09STIF1000 De
NF031F10STIF1000 De
EST506594 KV3 Medic
NF102E11EC1F1085 E1
NF101B04F1LF1031 Ph
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          3 601331677F2 NCI_CGA
0 T7 end of clone BB0
6 601808909F1 NCI_CGA
9 63070601.x1 C. rel
7 BB176997 REKEN full
7 BB320547 RIKEN full
7 AU024647 MOUSE unfe
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3 GA_Ea0018120f Gossypi
1 NF051806LF1F1045 Devel
6 MtBA44A1IF1 MtBA Medic
7 NF102E071NF1055 Insect
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                                                  About: Results were produced by the GenCore Copyright (c) 1993-2000 Compugen Ltd.
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Database: EST:*
Database sequences: 11351937
Database length: 1077921985
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| 3323<br>3323<br>3323<br>3323<br>3323<br>3323<br>3323<br>332                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 394                   |
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| b_est1: BB16<br>b_est1: BB16<br>b_est1: BB16<br>b_est1: BB16<br>b_est1: BB16<br>b_est1: BB16<br>b_est2: BG14<br>b_est2: BG16<br>b_est2: BG16<br>b_est                                        | est1:BE125            |
| AV249715 AV249715 RIKEN full-le AI975782 EST270376 Schistoscoma BF370117 RC5-FN0022-270700-033-AZ210976 AZ210976 AZ210976 AZ210976 AZ210976 AZ210976 AZ210976 AZ210976 AZ210977 LW0026N07F Wouse 10kb AZ310975 LW0026N07F Wouse 10kb AZ310975 LW0026N07F Wouse 10kb AZ310975 LW0026N07F Wouse 10kb AZ310975 LW0026N07F Wouse 10kb BE518841 WHE06066 E03 1062A When BE518841 WHENGC_9 BE79486 601342221F1 NILMGC_9 BE79486 601342221F1 NILMGC_9 BE79486 60134221F1 NILMGC_9 BE79486 60134221F1 NILMGC_67 BE79486 60134221F6F1 NILMGC_67 BE79486 60134221F7F1 NILMGC_67 BE79486 60134221F7FF1 NILMGC_67 BE79486 MUNICAL SACAPLE AZ312038 MUS MUSCALUS adult ma AZ812038 MUS MUSCALUS AUGLIO XI SCAREAGONE BE399796 BE399796 MUNICACAPL AZ312038 MUS MUSCALUS AUGLIO XI SCAREAGONE BE399796 BE3999796 BE399796 BE3999796 BE399997 BE3999796 BE3999796 BE3999796 BE399997 BE3999999999999999999999999999999999999                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         |                       |
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| 602714270FI NIH_MGC<br>602716448FI NIH_MGC<br>602716448FI NIH_MGC<br>EST491589 CSTS SOla<br>RNS MUSCULUA 10<br>11<br>RPCI.23 385/21.77 R<br>602716538FI NIH_MGC<br>602716538FI NIH_MGC<br>602716538FI NIH_MGC<br>602716538FI NIH_MGC<br>8027161410 MOUSE 9-<br>RYL.23-218471.79 R<br>1M002M12.31 NCI_CGAP<br>1M002M12.31 NCI_CGAP<br>602951360FI NIH_MGC<br>601315712FI NIH_MGC<br>601315712FI NIH_MGC<br>601315712FI NIH_MGC<br>601315712FI NIH_MGC<br>601290469FI NIH_MGC<br>601315712FI NIH_MGC<br>6012140708FI NIH_MGC<br>601216718163FI NIH_MGC<br>601216718163FI NIH_MGC<br>601214076FI NIH_MGC<br>601214076FI NIH_MGC<br>601214076FI NIH_MGC<br>601214076FI NIH_MGC<br>601214076FI NIH_MGC<br>601214076FI NIH_MGC<br>601216163FI NIH_MGC<br>601216163FI NIH_MGC<br>601216163FI NIH_MGC<br>601216163FI NIH_MGC<br>601216163FI NIH_MGC<br>60276647FI NIH_MGC<br>60276647FI NIH_MGC<br>60276647FI NIH_MGC<br>60276647FI NIH_MGC<br>60276647FI NIH_MGC<br>60276647FI NIH_MGC<br>6027667FI NIH_MGC<br>6026281FI NIH_MGC<br>60156818FI NIH_MGC<br>60156818FI NIH_MGC<br>601562817FI NIH_MGC                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 019458029F1 NTH_MGC. 00295035F1 NTH_MGC. 002947110F1 NTH_MGC. 002947110F1 NTH_MGC. 002947918F1 NTH_MGC. 002947918F1 NTH_MGC. 002947918F1 NTH_MGC. 002947918F1 NTH_MGC. 002943F1 NTL_CGA. 00109244F1 NTL_CGA. 00109244F1 NTL_CGA. 00109245F1 NTH_MGC. 00215546F1 NTH_MGC. 0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       |
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| 9b_est2:BG754881 9b_est2:BG755970 9b_est2:BG552316 9b_est2:BG552311 9b_est2:BG552311 9b_est2:BG56047 9b_est2:BG76047 9b_est2:BG76047 9b_est2:B1282272 9b_est2:B1282272 9b_est2:B1282732 9b_est2:B1282733 9b_est2:BG593805 9b_gss:AZ559365 9b_gss:AZ569669 9b_gss:AZ569669 9b_gss:BH112592 9b_est2:BG180175 9b_est2:BG180175 9b_est2:BG180175 9b_est2:BG180175 9b_est2:BG180130                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | gb_est2:BF03336<br>gb_est2:BF03336<br>gb_est2:BG748450<br>gb_est2:BI193139<br>gb_est2:BI194139<br>gb_est2:BI10443<br>gb_est2:BG765993<br>gb_est2:BF215613<br>gb_htc:AK005363<br>gb_htc:AK005363<br>gb_est2:BF215613<br>gb_est2:BF21503<br>gb_est2:BF2150<br>gb_est2:BF681220<br>gb_est2:BF681220<br>gb_est2:BF68123343<br>gb_est2:BF681230<br>gb_est2:BF681230<br>gb_est2:BF681230<br>gb_est2:BF681230<br>gb_est2:BF681230                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           |
| AM636315 vq76e12.s1 Knowles Sol<br>AW3636315 vq76e12.s1 Knowles Sol<br>BF098547 CM3-CM0092-201000-411-<br>AZ364562 1M0110E22R Mouse 10kb<br>BR016508 cw3-64008.s1 NCI_CGAP_LO<br>AZ455089 RPCI_24.y1 NCI_CGAP_GO<br>AZ455089 RPCI_24-6669.17 RPCI_2<br>BF13719 EST441309 tcmaco root,<br>AZ608572 RPCI_23-467121.TVB RPC<br>BF13719 EST441309 tcmaco root,<br>AZ608572 RPCI_23-467121.TVB RPC<br>AZ608572 RPCI_23-467121.TVB RPC<br>AZ608572 RPCI_23-467121.TVB RPC<br>AZ608572 RPCI_23-467121.TVB RPC<br>AZ608572 RPCI_23-467121.TVB RPC<br>AZ608572 RPCI_23-670121.AZ6<br>AZ608572 RPCI_23-670121.AZ6<br>AZ608572 RPCI_23-67014.35-<br>BE019758 GY0005.x1 Soares_Lota<br>AZ60834 tt45c01.x1 NCI_CGAP_GO<br>BF151823 u220912.y1 NCI_CGAP_CC<br>BF892786 QY1-RPCOSTS Solanum<br>AZ408358 HOM335C1R Mouse 10kb<br>BF151823 u220912.y1 NCI_CGAP_CC<br>AZ408358 HOM335C1R Mouse 10kb<br>BF255195 U1-R-AB1-ys-f-04-0-UI<br>BF151823 u220612.y1 NCI_CGAP_CC<br>AZ673498 HS_2061_AZ_F05_T7 CIT<br>BF131318 SAZ76_BZ_DO2_MR CIT<br>BG273498 BJ5110p.r1 Neurospora<br>BG273498 BJ510p.r1 Nourospora<br>BG273498 BJ510p.r1 Nourospora<br>BG273498 BJ510p.r1 Nourospora<br>AZ408675 ZM010210R MAULE tuber 1a<br>AW30178 wa32905.x1 NCI_CGAP_GC<br>AZ817820 MO087E05R Mouse 10kb<br>BG592028 Hy11d03.x1 NCI_CGAP_GC<br>AZ817820 MO087E05R Mouse 10kb<br>BG592028 Hy11d03.x1 NCI_CGAP_EC<br>BG889273 EST15124 CSTD Solanum<br>BE502028 Hy11d03.x1 NCI_CGAP_BC<br>BG313174 EST464634 tcmato crowr<br>BF033827 potato leave<br>BG3382670 x1 NCI_CGAP_EC<br>AZ817820 PO007801 potato leave<br>BG3382670 x1 NCI_CGAP_EC<br>AZ817820 PO007801 potato leave<br>BG3386957 EST343828 potato leave                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | ST321378 Comato F<br>MBACO7P137 PSU B<br>MBACO7P137 PSU B<br>1. F. B.D.O. aeg-a-09-<br>K35el.2. x1 zebrafi<br>8dlO.r. x1 zebrafi<br>8dlO.r. Scares_se<br>MO104K05F Mouse 1<br>MO104K05F Mouse 1<br>MO104K05F Mouse 1<br>MO104K05F Mouse 1<br>MO104K05F Mouse 1<br>MO104K05F Mouse 1<br>ST5505407 cSTS Sol<br>ST5505478 cSTS Sol<br>ST2505478 cSTS Sol<br>ST250694 Mormaliz-<br>ST2505478 cSTS Sol<br>ST2505478 cSTS Sol<br>ST2505478 cSTS Sol<br>ST3-EM0090-111200-<br>ST215_AL_H04_MR<br>K3-EM0090-111200-<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-SOL<br>ST3-                                                                                                                                                                                                                                                                                                                                                                       |
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| 9b est1:AA636315<br>9b_est2:BP989547<br>9b_est2:BP989547<br>9b_est2:BP989547<br>9b_est2:BP016508<br>9b_gss:AZ498513<br>9b_gss:AZ498513<br>9b_est2:BP1369503<br>9b_est2:BP1369503<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719<br>9b_est2:BP13719      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| BFF550641 UI-R-CO-hr-f-10-0-U T18664 h06019t Testis 1 Homo AA955081 UI-R-CO-gz-b-03-0-U AW777964 fk42d4, y1 zebrafis AW777964 fk42d4, y1 zebrafis AW777964 fk42d4, y1 zebrafis AW402527 UI-HF-BK0-aas-f-02- AW478499 20541 MARC 180V Bos AW834878 RC6-127003-17010-0 R22298 y22641 MARC 131299-0 R22298 y22641 NARC 131299-0 R22298 y22641 NARC 1900-0 R22298 y22641 NARC 1900-0 RY41099 W169902 x1 NCI CGAP BE099237 UI-R-BJ1-atz-h-10-0 RY41099 W169902 x1 NCI CGAP BE099237 UI-R-BJ1-atz-d-0-0-U RY562496 UI-R-AA0-af-c-12-0 RY41099 W19-W-8-9-11-0 RY5651 y44802 x1 Scares fet RY706257 HS-555_Al_E08_TA RY001725 HS-555_Al_E08_TA RY0065179 PM3-HN0076-02404_SPEE RY0061996 UI-R-BJ1-atI11-0 RY6853879 maa72h09 y1 Scares inf AI704112 UI-R-BU1-atI11-0 RY453379 maa72h09 y1 Scares AC706257 HS-5500-0 RY491740 SHA5075-AL_F03_B RY33134 UI-R-BU0-ane-c-05-0 RY491710 SHA50605 x1 NCI_CGA RY491710 SHA50605 x1 NCI_CGA RY491710 SHA50605 x1 NCI_CGA RY491710 SHA50605 x1 NARC 180V Bos RY718652 287396 MARC 180V Bos RY718652 287396 MARC 380V Bos RY7186501 UI-R-BU-COF_TA RY49170 SHA913-COF_TA RY49170 SHA913-CH-U-TO-MARC 180V RY49170 SHA913-CH-U-TO-MARC 180V RY49170 SHA913-CH-U-TO-MARC 180V RY49170 SHA913-CH-U-TO-MARC 190V RY49170 SHA913-CH-U-TO-MARC 190V RY49110 UI-R-BU-COF_TA RY49110 UI-R-BU-COF_TA RY49110 UI-R-BU-COF_TA RY49110 UI-R-BU-COF_TA RY61110 UI-R-BU-COF_TA                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | AW/8944 CUISOS-F Lamanda Lap<br>BF558842 UI-R-AI-dv-c-10-0-U<br>BE850842 UI-R-AI-dv-c-10-0-U<br>BE850142 UW13405.91 Soares m<br>AW494484 UI-M-BH3-aum-h-03-0<br>AW494484 UI-M-BH3-aum-h-03-0<br>AW494484 UI-M-BH3-aum-h-03-0<br>AW497370 RPCI-24-228F13.TJ R<br>AAI70595 ms84f09.rl Soares m<br>AAI70595 ms84f09.rl Soares m<br>AAI3880 mt21b04.rl Soares m<br>AAI3132 AW1053H05R MOUSE 10<br>AX851326 AW1053H05R MOUSE 10<br>AX855568 96902 WARC 1BV BOS<br>BF471916 UI-M-BH3-awp-c-02-0<br>AM659568 96902 WARC 1BV BOS<br>BR471916 UI-M-BH3-awp-c-02-0<br>AM631002 UI-R-CO-je-e-10-0-U<br>AX870241 2W0182H09R MOUSE 10<br>AV603807 AV603907 BOS taurus                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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| BED054797 GA_E00031G19f Gossypl<br>BIO087162 602850842F1 NIH_MGC_1G<br>AL5138016 AL513809 LTT_RFL0013_FB1<br>AL513809 AL513809 LTT_RFL0013_FB1<br>BG107106 602291010F1 NIH_MGC_8<br>AL213801 F0202179F1 NCI_CGAP_1GAP_1GAP_1GAP_1GAP_1GAP_1GAP_1GAP_1                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  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| 1241FI NIH<br>125241FI NIH<br>12651 NIH<br>12661 N                     | AL026188 Fugu rubripes GSS s<br>AQ384386 RPCI11-139L2.TJ RPC<br>AV088994 AV088994 Wus muscul<br>BB308036 BB308036 RIKEN full             |
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| 1112.5.59<br>1112.5.70<br>1112.5.33<br>1112.5.33<br>1112.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5.33<br>1113.5                   | 119.06<br>118.90<br>118.87<br>118.87                                                                                                     |
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| gb_est2:BE889980 gb_gss:AQ573945 gb_est2:W08409 gb_est2:W08409 gb_est2:W08409 gb_est1:AL561129 gb_est1:AL561129 gb_est1:AL561129 gb_est1:AR020369 gb_gss:AQ362332 gb_gss:AQ362332 gb_gss:AQ362332 gb_gss:AQ362332 gb_gss:AQ362332 gb_gss:AQ362332 gb_gss:AQ362332 gb_est2:BE871354 gb_gss:CNS0GGA gb_gss:AZ52590G gb_gst1:BB415746 gb_gss:AZ52590G gb_gst1:BB415746                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | gb_gss:FR0029819<br>gb_gss:AQ384386<br>gb_est1:AV088994<br>gb_est1:BB308036                                                              |
| BH056025 RPCI-24-365A16.TJ RPCI<br>AQ772888 HS_2558_A2_B02_AR CIT<br>BF660799 maa72h09.x1 Soares mou<br>AA382398 HM0139106R Mouse 10kb<br>AA367220 vz39h09.r1 Soares mou<br>AA367220 vz39h09.r1 Soares mou<br>AA367220 vz39h09.r1 Soares mou<br>AZ487901 IM012BC19.F MXSI (N<br>AQ47221 RPCIII-35P16.TJ RPER PRCI-<br>AZ487901 IM01317B20R Mouse 10kb<br>AG014210 RPCIII-35P16.TJ RPER PRCI-<br>AZ487901 IM01317B20R Mouse 10kb<br>AG014324 DKPCZHO-SOE TABE RPCI-<br>AZ61879 IM0455016F Mouse 10kb<br>BE755889 209768 MARC 2BOU BOS t<br>AL6040324 DKFZP4441NI13_r1 434 (A<br>AZ375161 IM0128C19F MOUSE 10kb<br>AZ67163 EST23728 NOTMAILI3C A<br>AZ67163 EST23728 NOTMAILI3C A<br>AZ67163 EST23728 NOTMAILI3C A<br>AZ67163 EST23728 NOTMAILIZED T<br>AZ67163 EST23619 NOTMAILIZED T<br>AZ67163 EST23619 NOTMAILIZED T<br>AZ67163 EST23619 NOTMAILIZED T<br>AZ67163 EST23619 NOTMAILIZED T<br>AZ67163 AL508613 HOTGOUN VUJO<br>AZ67164 AL508613 HOTGOUN VUJO<br>AZ686083 AU0167802 NOTMAILIZED T<br>AZ67163 AL508613 HOTGOUN VUJO<br>AZ686083 AU0167802 NOTMAILIZED T<br>AZ67163 AL508613 HOTGOUN VUJO<br>AZ686083 AU0167802 NOTMAILIZED T<br>AZ67163 AL508613 HOTGOUN VUJO<br>AZ66009 EMC27722 NOUSE 10kb<br>AZ2816607 AU0167802 NOTMAILIZED T<br>AZ67167 NOTMAILIZED T<br>AZ67167 NOTMAILIZED T<br>AZ67167 NOTMAILIZED T<br>AZ67167 NOTMAILIZED T<br>AZ686083 AU0167802 NOTMAILIZED T<br>AZ67167 NOTMAILI                                                                                                                                                                         | AL583372 AL583372 LTL_NFL010_BG<br>AL187032 SP_1008_A2_E06_T7A Str<br>BI104631 6028915038T NCI_CGAP_I<br>BG246037 602358866F1 NCI_CGAP_M |
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| 9b_9ss: BH056025<br>9b_9ss: AQ772888<br>9b_9ss: AQ772888<br>9b_9ss: AQ772888<br>9b_9ss: AQ772808<br>9b_9ss: AQ7700<br>9b_est2: C78770<br>9b_9ss: AQ487021<br>9b_9ss: AQ487021<br>9b_9ss: AAG21879<br>9b_9ss: AAG21879<br>9b_9ss: AAG21879<br>9b_est1: AM944238<br>9b_est1: AM944238<br>9b_est1: AAM92364<br>9b_est1: AAM92364<br>9b_est1: AAM92364<br>9b_est1: AAM92364<br>9b_est1: AAM933130<br>9b_est1: AAM9331310<br>9b_est1: AAM9331310<br>9b_est1: AAM9331310<br>9b_est1: AAM9331310<br>9b_est1: AAM933130<br>9b_est1: AAM9331310<br>9b_est1: AAM9331310<br>9b_est1: AAM9331310<br>9b_est1: AAM933130<br>9b_est1: AAM933130<br>9b_est2: BG6801336<br>9b_est2: BG781479<br>9b_est2: BG781479<br>9b_est2: BG781479<br>9b_est2: BG7814360<br>9b_est2: BG7814360<br>9b_est2: BG7814360<br>9b_est2: BG7814360<br>9b_est2: BG7814360<br>9b_est2: BG7814360<br>9b_est2: BG7814360<br>9b_est2: BG7814360<br>9b_est2: BG781336<br>9b_est2: BG781336<br>9b_est2: BG781336<br>9b_est2: BG781336                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | gb_est1:AL583372<br>gb_gss:AZ187032<br>gb_est2:BI104631<br>gb_est2:BG246037                                                              |

| D26782 CELK002D6R Yuji Kohar AA147516 z150f02.r1 Soarea.p BE446737 WHE1140_H11_P222S W BE446737 WHE1140_H11_P222S W BE471720 UI-M-BH31-avv-c-08-0 BF523343 M35H10STM Arabidopus BE5237 yb97h11.s1 Stratagene BE186864 946013710.x1 946 - AZ837155 2M013ZL17F Mouse 10 BG989934 PM2-H1171-210101-0 BE481504 L66978 BAAC SEOV Bo AR815413 aud2d05.y1 Schneide AZ837155 2M013ZL17F Wuji Kohar B181608 CELK033E4R Yuji Kohar D33608 CELK033E4R Yuji Kohar D33608 CELK033E4R Yuji Kohar D33608 CELK033E4R Yuji Kohar D33608 CELK032E4R Yuji Kohar D33608 CELK016ZR Yuji Kohar D33608 CELK016ZR Yuji Kohar D33608 CELK016ZR Yuji Kohar D3469901 UI-M-BH3-atw-h-12-0 BF808552 CUI-M-10002-141100-0 BF808552 CUI-M-10002-141100-0 BF808552 CUI-M-10002-141100-0 BF808552 CUI-M-10002-141100-0 BF808555 UI-M-1000-1 BF80855 UI-M-1000-1 UI-M-1000-1 BF80855 UI-M-1000-1 UI-M-10                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | AZY81/17 ZMCAZETEK MOUSE UU BH112105 RPCT-24-402023 TU R AA996934 UT-R-C0-hj-g-09-0-U AI34177 GQ942010.x1 Soares_t AM373246 RCS-BT00508-031299-0 BED02386 hz18b09.x1 NCL_CGAP AZ829359 RPCT-23-163018.TJ R AA610527 np91f07.s1 NCL_CGAP AZ819355 RPCT-23-163018.TJ R AA610527 np91f07.s1 NCL_CGAP AX819355 AM091F24R MOUSE 10 AW791613 D00699-R Lambda Zap AQ836747 HS_5500_AZ_B06_SP6E BF468784 UI-M-BH3-atn-d-07-0                                                                                                    |
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| 9b_est2: D26782  9b_est1: AA147720  9b_est1: BE4447720  9b_est2: BF651413  9b_est2: BF651413  9b_est2: BF651413  9b_est2: BF651413  9b_est2: AB37155  9b_est2: AB37155  9b_est2: AB371608  9b_est2: BF606706  9b_est1: AA018787  9b_est2: BF606706  9b_est2: BF60670                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 9b.958:A28112105 9b.958:BH111105 9b.est1:AA996934 9b.est1:AA341757 9b.est1:AM334757 9b.est2:BI073756 9b.est2:BI073756 9b.est1:BE502586 9b.gss:AZ29959 9b.est1:AA610527 9b.gss:AZ2926323 9b.est1:AA791613 9b.gss:AZ819956 9b.gss:AZ819956 9b.gss:AZ819956 9b.gss:AZ819956 9b.gss:AZ819956                                                                                                                                                                                                                                |
| CM2-NT01<br>100052452<br>8112911.<br>8129213.<br>8129213.<br>8129213.<br>8129213.<br>8129213.<br>8129213.<br>8129213.<br>8129213.<br>8129213.<br>8129243183<br>8129243183<br>8129243183<br>81202023.<br>81202023.<br>81202023.<br>81202023.<br>81202023.<br>8120203.<br>8120203.<br>8120203.<br>8120203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81203.<br>81 | ALREAGOS WHELES, AND.—ADUSES SECA ALREAGOS WHELES, AND.—ADUSES SECA ALREAGOS XI NCI CGAP_BL D34312 CELKO44B4R Yuji Kohara U BF324709 SUJ4004.91 Zebrafish a AW174580 fj05h10.91 Zebrafish a AW174580 fj05h10.91 Zebrafish a AW174580 fj05h10.91 Zebrafish a AW174580 fj05h10.91 Zebrafish a AW174580 fy05h10.91 Zebrafish BE523805 M41H125TM Arabidopsis BE523805 M41H125TM Arabidopsis BC5784 CELKOO7742R Yuji Kohara U BC604580 WHE0947_C10_F192S Whea AW075094 xa68807.x1 NCI_CGAP_HS AR232589 zr28b08.r1 Stratagene |
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| 9b_est2:BF925624<br>9b_gss:Ax3289570<br>9b_gss:Ax3289570<br>9b_est1:BB339475<br>9b_est1:BB295953<br>9b_est1:BB295953<br>9b_est2:BF3296<br>9b_est2:BF32101<br>9b_est2:BF341163<br>9b_est2:BF341163<br>9b_gss:TA48008P<br>9b_gss:TA48008P<br>9b_gss:TA48008P<br>9b_gss:TA48008P<br>9b_gss:TA48008P<br>9b_gss:TA48008P<br>9b_est2:BF00450<br>9b_est2:BF00450<br>9b_est2:BF00450<br>9b_est2:BF00450<br>9b_est2:BF00450<br>9b_est2:BF00490<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2:BF10050<br>9b_est2                                                                                                                    | 9b_est1:N1887059 9b_est2:D34312 9b_est2:D34312 9b_est2:BR324709 9b_est1:MN74580 9b_est1:MN216186 9b_est1:AN3180143 9b_est1:AN3180143 9b_est1:BB523805 9b_est2:D26784 9b_est2:BG604580 9b_est1:AN332589                                                                                                                                                                                                                                                                                                                  |

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BF268018 844 bp mRNA EST 09-MAR-2001
HV_CEa0019J17f Hordeum vulgare seedling green leaf EST library
HV_CEA0019J17f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                          Hordeum vulgare
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; Liliopsida; Poales; Poaceae; Pooldeae
; Triticeae; Hordeum.
1 (bases 1 to 844)
Wing, R., Close, T.J., Kleinhofs, A., Wise, R., Begum, D., Frisch, D., Yu, Y., Anderson, H., Dale, J., Henry, D., Kernodle, S., Palmer, M., Rambo Wood, T., Saski, C., Schwartzbeck, J., Slmmons, J., Choi, D. W., Main, D. and Wood, T.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /note="Vector: lambdaZAP; Site_1: EcoR1; Site_2: Xhol; For more details on library preparation and sequence analysis see http://www.genome.clemson.edu/projects/barley/ To order a clone see http://www.genome.clemson.edu/orders" 290 c 276 g 128 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Development of a genetically and physically anchored EST resource for barley genomics for barley genomics for barley genomics for both barley genomics on Nov 17, 2000) on Nov 17, 2000 this sequence version replaced gl:11199013.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /clone="HV_CEMO19J17f"
/clone_lib="Hordeum vulgare seedling green leaf EST
library HvCDNA0004 (Erysiphe infected & control)"
/tissue_type="seedling green leaf"
/lab_host="TJC121"
174 GACGAGTTGCTGGCGCGTTGGGGTACAAGGTTCGTGCTTCCGACATGGC 223
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Clemson University Genomics Institute
Clemson University
100 Oordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1. .844 // Apparlsm="Hordeum vulgare" // Cultivar="CII6155 (Mla13)" // Ab_xref="taxon:4513"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Seg primer: AATTAACCCTCACTAAAGGG
High quality sequence stop: 587.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: rwing@clemson.edu
                                                                                                                                                                                                                                                                                                 BF268018.2 GI:13263734
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US-09-485-529-104 x BF268018
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Ratio: 4.765
Percent Similarity: 100.000
                                                                                                                             seq_name: gb_est2:BF268018
                                                                                                                                                                      seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                             barley
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                                                                                 224 T 224
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                 AF083303 AF083303 Drosophila me
AI94302 qy98e10 x1 NCI_CGAP_Br
BH085545 RCI-24-310A2.TV RPCI-
AQG7492 HS_2161_A1_H01_T7C_CII
AWS86740 EST318363 MHAM Medicag
BF497115 AT11189.5prime AT Dros
AZ344778 IM0079802F Mouse 10kb
AQ037915 CIT-HSP-2325G5_TV CIT-
AA394318 25915 Lambda-PRLZ Arak
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /Lissue_type="Geed coats"
/Lissue_type="Geed coats"
/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI; This conA library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developemental stage, average fresh weight 250 map per seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adopters were ligated to the blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amphilied once using E. coli host strain XLI Blue MRF'. Inserts were then subcloned by mass excision using ExAssist helper phage for conversion into phagemid vector pBK-CMV in E. coli host
                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryophyta; Tracheophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                                                                                                                                                                                                                                                                                                 06-SEP-2000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Agriculture and Agri-Food Canada
1391 Sandford Street, London, Ontario, Canada NSV 4T3
TTE1: 519 457 1470
Fax: 519 457 3997
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Gaps: 0
Percent Identity: 100.000
                                                                                                                                                                                                                                                                                  BE659955 711 bp mRNA EST
1077 GmaxSC Glycine max cDNA, mRNA sequence.
BE659955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seed
  Harris, N., Chapman, B.P. and Gijzen, M. Gene expression in developing soybean Unpublished (2000)
Contact: Gijzen M
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3.5e+03
                                                             .5e+03
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Location/Qualifiers
1. 711
/ Organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_lib="GmaxSC"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      from: 1 to: 711
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114.05
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37.00
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US-09-485-529-104 x BE659955
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Percent Similarity: 100.000
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LOCUS
BE659955
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                   gb_est1:AF083303
gb_est1:AI494302
gb_gss:BH085545
gb_est1:AK586740
gb_est2:BF497115
gb_gss:A734478
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                                                                                                                                                                      gb_gss:AQ037915
gb_est1:AA394318
gb_est2:BF558068
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VERSION
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TITLE
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Align seg 1/1 to: BF268018 from: 1 to: 844
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Length: 17 Gaps: 0 Percent Identity: 100.000

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legume, Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
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Percent Similarity: 100.000'
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US-09-485-529-104 x AV410222
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Sukaryota, Viridiplantae, Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from a
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                                                                                                                                                                   11-NOV-1994
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AV410222 Lotus japonicus young plants (two-week old) Lotus
japonicus cDNA clone MWL069f02_r 5', mRNA sequence.
                                                                                                                                                             D39460 263 bp mRNA EST 11-N
RICSO803A Rice shoot Oryza sativa cDNA, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          , mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
/clone_lib="Rice shoot"
/note="Etiolated shoot (8 days old)"
/ 64 c 116 g 35 t 2 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Ratio: 4.588 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   /organism="Oryza sativa"
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                                                                                                                                                                                                                                                        D39460.1 GI:568611
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US-09-485-529-104 x D39460
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                                                              seq_name: gb_est2:D39460
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                                                                                                                                                                                                                                                                                                                                                          Oryza sativa
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Medicago truncatula insect herbivory library
Lingublished (2000)
Longuished (2000)
L
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/organism="Lotus japonicus"
/db_xref="taxon:34305"
/db_xref="taxon:34305"
/clone="Walt069f02_r"
/clone="lib="Lotus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/dote="Vector: plluescriptII SK-; Site_1: EcoRI; Site_2:
XhoI; isolate=Miyakojima MG-20"

44 a 70 c 101 g 90 t
                                                                                                                                                      The First Laboratory for Plant Gene Research Kazusa DNA Research Institute Yana 1532-3, Kisarazu, Chiba 292-0812, Japan Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Spermatophyta; Magnollophyta; eudocae; Papillonoideae; Trifolleae;
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LOCUS BE321891 372 bp mRNA EST 21-DEC-2000
DEFINITION NF045B07IN1F1058 Insect herbivory Medicago truncatula cDNA clone
NF045B07IN 5', mRNA sequence.
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Gaps: 0
Percent Identity: 94.118
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DNA Res. 7 (2), 127-130 (20
20277479
Contact: Yasukazu Nakamura
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Quality:
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JOURNAL
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                     /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF045B071N"
/clone=11b="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vero: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

33 a 66 c 72 g 81 t
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Location/Qualiflers
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Percent Identity: 94.118
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/cultivar="Nipponbare"
/db_xref="taxon:4530"
/clone="C51976_1A"
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102 c 134 g
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Percent Similarity: 100.000
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US-09-485-529-104 x BE321891
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LOCUS C27475
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source
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KEYWORDS
SOURCE
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/tissue_type="root tips"
/dev.stage="harvested after 3 days of N-starvation"
/dev.stage="harvested after 5 days of N-starvation"
/dev.stage="harvested after 5 site_1: ECRI; Site_2:
XhoI: Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). CDNA
was prepared from polyA+ enriched RNA. The CDNA was
directionally ligated into Uni-zapxR vector from
Stratagene and packaged using Giapaex Gold packaging
extracts. Plasmids containing CDNA inserts were
mass-excised from phage stocks using Exhasit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
74 C 75 9
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Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  AL369357 399 bp mRNA EST 03-AUG-2000 MtBA30E09F1 MtBA Medicago truncatula cDNA clone MtBA30E09 T3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Genoscope - Centre National de Sequencage
BP 191 91006 EVRX cedex - France
BP 191 91006 EVRX cedex - France
Email: seqref@genoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 399)
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P. Medicago truncatula ESTs from nitrogen-starved roots
                                                                                                                                                                                                                                                                                                Length: 17
Gaps: 0
Percent Identity: 94.118
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1. 399
/organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="texon:3880"
/clone="MtBA30E09"
                                                                                                                                                                                                                                  Align seg 1/1 to: C27475 from: 1 to: 388
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="MtBA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AL369357
AL369357.1 GI:9669110
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula
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                                     Ratio: 4.588
Percent Similarity: 100.000
      78.00
                                                                                                                                                                     US-09-485-529-104 x C27475
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: gb_est1:AL369357
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_documentation_block:
LOCUS AL369357
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alignment\_scores:

alignment\_scores:

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seq_name: gb_est1:AL369482
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DEFINITION
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Eukaryota: Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta: Magnoliophyta; Liliopsida; Poales; Poaceae;
Enrhartoideae; Oryzaee; Oryzae.

E (bases 1 to 399)
S Saski, T. and Yamamoto, K.

Rice cDNA from immature leaf including apical meristem (2000)
Unpublished (2000)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
305-8602, Japan
Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 /clone_lib="Rice cDNA from immature leaf including apical meristem (under short day condition)"
//dev_atage="immature leaf including apical meristem (under short day condition)"
//dev_atage="immature leaf including apical meristem (under short day condition)"
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LOCUS AU091413 399 bp mRNA EST 05-JUN-2000
DEFINITION AU091413 Rice cDNA from immature leaf including apical meristem
(under short day condition) Oryza sativa cDNA clone E60220, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  285 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTTCGCTCTTCCGACATGGC 334
                                                                                                                                                                             1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                  Gaps: 0
Percent Identity: 94.118
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Percent Identity: 94.118
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                                                                                                                                          to: 399
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/db_xref="taxon:4530"
/clone="E60220"
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                                                                                                                                          from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AU091413.1 GI:8251089
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US-09-485-529-104 x AU091413
                                                                                                US-09-485-529-104 x AL369357
                                                                                                                                      to: AL369357
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Percent Similarity: 100.000
                  Ratio: 4.588
Percent Similarity: 100.000
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78.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Oryza sativa.
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  Quality:
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/dev_stage="harvested after 3 days of N-starvation"
/dev_stage="harvested after 3 days of N-starvation"
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Xhoi; plants were grown in an aeroponic chamber for 14
days on nitrogen rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The CDNA was
directionally lighted into Uni-zapKR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from page stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
                                                                                                                                                                                                                                                         Medicago truncatula
bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                           AL369482 458 bp mRNA EST 03-AUG-2000
MtBA31D06F1 MtBA Medicago truncatula cDNA clone MtBA31D06 T3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Contact: Genoscope - Centre National de Sequencage
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
Email: Seqrefégenoscope.cns.fr, Web: www.genoscope.cns.fr
Contact: Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Woleculaire des Relations Plantes-Microorganismes,
CNR-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                                        Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O., Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Medicago truncatula ESTs from nitrogen-starved roots Unpublished (2000)
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Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /cultivar="Jemalong"
/db_xref="taxon:3880"
/clone="MtbA31006"
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                                                                                                                                                             AL369482.1 GI:9669235
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US-09-485-529-104 x AL369482
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Percent Similarity: 100.000
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seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                              Medicago.
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Ratio:
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KEYWORDS
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/dev_stage="harvested after 3 days of N-starvation"
/dev_stage="harvested after 3 days of N-starvation"
/dev_stage="harvested after 1 bsk; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). cDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapXR vector from
Stratagene and packaged using Gigapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
83 a 93 c
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                           AL371425 466 bp mxna .... MtBA44B05F1 MtBA Medicago truncatula cDNA clone MtBA44B05 T3, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
BP 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
BR 191 91006 EVRY cedex - France
Contact : Pascal Games and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INNA, BP 27 31326 Castanet-Tolosan Cedex, France (Email :
Mt-estétoulouse.inra.fr Website : http://sequence.toulouse.inra.fr/Mtruncatula.html).
                                                                                                                                                                                                                                                                                                                                                                                                                                   1 (bases 1 to 466)
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Niebel, A., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
, V. and Gamas, P.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Medicago truncatula ESTs from nitrogen-starved roots Unpublished (2000)
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Percent Identity: 94.118
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                                                                                                                                                                                                                                                     AL371425.1 GI:9671178
                                                                                                                                                                                                                                                                                                                         Medicago truncatula
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Percent Similarity: 100.000
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                                                                                       seq_name: gb_estl:AL371425
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Ratio:
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ORIGIN
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KEYWORDS
SOURCE
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Lotus japonicus.
Lotus japonicus
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
                                                                                                                                                                                                                                           Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; Liliopsida; Poales; Poaceae;
Ehrhartoideae; Oryzeae; Oryza.
                                                            30-JUL-2001 A07 bp mRNA EST 30-JUL-2001 AU222715 Rice shoot Oryza sativa cDNA clone S0583, mRNA sequence. AU222715
                                                                                                                                                                                                                                                                                                               1 (bases 1 to 467)
Sasaki, T. and Yamamoto, K.
Rice DNA from etiolated shoot (2001)
Unpublished (2001)
Contact: Takuji Sasaki
National Institute of Agrobiological Resources
Rice Genome Research Program, Kannondai 2-1-2, Tsukuba, Ibaraki
Tel: 81-298-38-7441
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Email: tsasaki@abr.affrc.go.jp, URL:http://rgp.dna.affrc.go.jp/
PROJECT = 'RGP'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        AV422153 484 bp mRNA EST 23-MAY-2000 AV422153 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWM005b04_r 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      /strain="Nipponbare, sub_species Japonica"
/db_xref="taxon:4530"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /clone_lib-"Rice shoot"
/note="Etiolated shoot (8 days old)"
136 c 176 g 65 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1. .467
/organism="Oryza sativa"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Location/Qualifiers
                                                                                                                                         AU222715.1 GI:15008327
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone="S0583
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Fax: 81-298-38-7468
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US-09-485-529-104 x AU222715
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Percent Similarity: 100.000
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seq_name: gb_est1:AU222715
                                                                                                                                                                                                Oryza sativa.
Oryza sativa
                                                  seq_documentation_block:
LOCUS AU222715
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/organism="Medicago truncatula"
/db_xref="taxon:3880"
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AW695914.2 GI:11957271
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Percent Similarity: 100.000
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barrel medic.
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LOCUS AW695914
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SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
                                                                                                                                                                                                                                                                                        The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /organism="Lotus japonicus"
/db_xref="taxon:34305"
/db_xref="taxon:34305"
/clone="MwM005b04_r"
/clone="MwM005b04_r"
/clone="MwM005b04_r"
/clone="hwm005b04_r"
/clone="hwm005b04_r"
/clone="totus japonicus young plants (two-week old)"
/dev_stage="young plants (two-week old)"
/note="Young plants (two-week old)"
/note="Yourge plants (two-week old)"
/note="Yourge plants (two-week old)"
/note="Young plants (two-week old)"
/note="
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He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
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On Apr 14, 2000 this sequence version replaced gi:7572088.
Contact: Dixon RA
1 (bases 1 to 484)
Asamizu, E., Nakamura, Y., Sato, S. and Tabata, S.
Generation of 7137 non-redundant expressed sequence tags from a DNA Res. 7 (2), 127-130 (2000)
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
1510 San 17302
Fax: 580 221 7380
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Percent Identity: 94.118
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                                                                                                                                                                                                                                                                       Contact: Yasukazu Nakamura
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                AW697326.2 GI:11933520
EST.
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US-09-485-529-104 x AV422153
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Ratio: 4.588
Percent Similarity: 100.000
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DEFINITION
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MEDLINE
COMMENT
                                                                                                        AUTHORS
TITLE
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KEYWORDS
SOURCE
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bel
C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7570676.
                                                                                                                                                                                                                                                                                 /dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
internodal stem segments"
120 c 87 g 131 t
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Gaps: 0
Percent Identity: 94.118
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The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402,
TTel: 580 221 7302
Fax: 580 221 7380
                                                                                                                        1. 537
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF17E1085"
/clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Email: radixon@noble.org
Insert Length: 654 Std Error: 0.00
Plate: 099 row: H column: 09
Seq primer: TCACACAGGAAACAGCTATGAC.
Location/Qualifiers
Email: radixon@noble.org
Insert Length: 686 Std Error: 0.00
Plate: 117 row: E column: 10
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
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isolated pod walls were collected and immediately frozen
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US-09-485-529-104 x BI308816
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Ratio: 4.588
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: gb_est1:AW694061
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KEYWORDS
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COMMENT
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudlcotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
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Grusak, M.A., Samac, D.A., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.

ESTS from developing reproductive tissues of Medicago truncatula Unpublished (2001)
Contact: Michael A. Grusak
USDA/ARS Children's Nutrition Research Center
Baylor College of Medicine
1100 Bates Street, Houston, TX 77030-2600, USA
TTel: 713-798-7078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /db_xref="taxon:3880"
/clone="pGPOD-8H2"
/clone="pGPOD-8H2"
/clone="toPOD"
/tissue_type="immature pod walls"
/dev_stage="Immature pods, ranging in age from 15 to 30
days after pollination"
/note="vector: pBluescript SK-; Site_1: EcoRI; Site_2:
EcoRI; EcoR
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BI308816 614 bp mRNA EST 20-JUL-2001
EST530226 GPOD Medicago truncatula cDNA clone pGPOD-8H2 5' end,
                     /clone_lib="boveloping stem"
/tissue_type="stem"
/dev_stage="pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
121 c 83 g 158 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TIGR sequence name: MTOAX37TK
More information is available at: www.medicago.org
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 94.118

    .614
    /organism="Medicago truncatula"
/cultivar="A17"

                                                                                                                                                                                                                                                                                                                                                                                 Length:
/clone-"NF099H09ST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Email: mgrusak@bcm.tmc.edu
B395671e
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-485-529-104 x AW695914
                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 4.588
Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                             78.00
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BI308816
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: gb_est2:BI308816
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                                                                                                                                                                                                                                                                                                                                             alignment_scores:
Quality:
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ORGANISM
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ORIGIN
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JOURNAL
COMMENT
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in liquid nitrogen. Pod walls were pooled for mRNA extraction. CDNA was prepared from polyA+ enriched RNA. The CDNA was directionally ligated into the Unisap XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-Zap phage using Ex-assist helper phage and propogated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago.
1 (Dasea 1 to 655)
14 (A. -Z., Shadle, G., Scott, A. D., Harris, A. R., Gonzales, R. A., Bell, C. J., Flores, H. R., Inman, J. T., Weller, J. W., May, G. D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       AW694061 655 bp mRNA EST 15-JUN-2000 NF072A05ST1F1036 Developing stem Medicago truncatula cDNA clone NF072A05ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  236 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTTCGCTCTTCCGACATGGC 285
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Email: radixon@noble.org
                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF072A05ST"
/clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: radixon@oble.org
Insert Length: 655 Std Error: 0.00
Plate: 072 row: A column: 05
Seq primer: TCACACAGAAACAGCTATGAC.
Location/Qualifiers
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to: 656

from: 1

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305 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTTCGCTCTTCCGACATGGC 354
                                                                           1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl
US-09-485-529-104 x AW694064
                                     to: AW694064
                                                                                                                                                                                                                               seq_name: gb_est1:AW696350
                                                                                                                                                                                                                                                                                                                                                                                                     barrel medic.
                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Medicago.
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                                     Align seg 1/1
                                                                                                                                                                                       355 T 355
                                                                                                                                                   17 a 17
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                                                                                                                                                                                                                                                                                                         DEFINITION
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                                                                                                                                                                                                                                                                                                                                                                 VERSION
KEYWORDS
SOURCE
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Darrel medic.
Medicago truncatula
Medicago truncatula
Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Mosidae; eurosids I; Fabales; Fabaceae; Papillonoideae; Trifolleae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 (bases 1 to 656)
He, X.-2., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell
, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Mobublished (2000)
Contact: Dixon RA Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW694064 656 bp mRNA EST 15-JUN-2000 NF072A07STIF1052 Developing stem Medicago truncatula cDNA clone
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
145 c 107 g 166 t
                                                                                                                                                                                                                                               Length: 17
Gaps: 0
Percent Identity: 94.118
                                                                                         Gaps: 0
Percent Identity: 94.118
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1. 656
/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF072A0751"
/clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Email: radixonenoble.org
Insert Length: 656 Std Error: 0.00
Plate: 072 row: A column: 07
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                           to: 655
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF072A07ST 5', mRNA sequence.
                                                                                                                                                                                                         Align seg 1/1 to: AW694061 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW694064.1 GI:7568803
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality: 78.00
Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                                     US-09-485-529-104 x AW694061
                                                                                         Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                       seq_name: gb_est1:AW694064
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LOCUS AW694064
                                                                         Quality:
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                                                       alignment_scores:
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VERSION
KEYWORDS
SOURCE
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ORIGIN
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Medicago truncatula
Medrayota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae;
                                                                                                                                                                                                                                                                                                                      1 (bases 1 to 667)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                               Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000)
AW686350 667 bp mRNA EST 15-JUN-2000 NF107A12ST1F1088 Developing stem Medicago truncatula cDNA clone NF107A12ST 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Ear: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Length: 17
Gaps: 0
Percent Identity: 94.118
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/db_xref="taxon:3880"
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/clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Email: radixon@noble.org
Insert Length: 667 Std Error: 0.00
Plate: 107 row: A column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AW696350 from: 1 to: 667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             internodal stem segments
147 c 126 g 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Location/Qualifiers
1..667
                                                                                                              AW696350.1 GI:7571200
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US-09-485-529-104 x AW696350
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity: 100.000
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367 T 367

304 T 304

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/organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Plant Biology Division
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
Tel: 580-221-5810
Fax: 580-221-7380
Email: mjharrison@noble.org
Chter name: MHAW-Zd-H09; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at 'http://chrysie.tamu.edu/medicago'.
Seq primer: T3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /tissue_type="roots colonized with Glomus versiforme" Adev_stage="Roots harvested at 10, 17, 22, 31 and 38 days post-inoculation with Glomus versiforme. The library was made from a mixture of RNA from each of these stages."
                                                                                                                                                                                                                                            Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
I (bases I to 701)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
ESTS from roots of Medicago truncatula after colonization with
                                                                                  AWS84661 701 bp mRNA EST 07-SEP-2000 N210765e MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone MHAM-2P18, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /ciltivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="MHAM-2P18"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /clone_lib="MHAM"
                                                                                                                                                                                         AW584661.1 GI:7261715
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Unpublished (2000)
Contact: Harrison M.J.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio: 4.588
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                    Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          library"
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     seq_name: gb_est1:AW584661
                                                           seq_documentation_block:
LOCUS AW584661
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KEYWORDS
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /Lissue_type="roots colonized with Glomus versiforme"
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-incculation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host-"E. coll strain XLOLR"
/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xho1; cDNA was prepared from polyA+enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-inoculation with Glomus versiforme. The cDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Glapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Fax: 580-221-738.
Email: mjharrison@noble.org
Other name: MHAM-2c-H09; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at _http://chrysie.tamu.edu/medicago'.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                                                                    Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Eukaryota; mixed EST libraries.
I (bases 1 to 683)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D.,
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
Glomus versiform
Unpublished (2000)
Ontact: Harrison M.J.
                                                AM584593 683 bp mRNA EST 07-SEP-2000 N210669e MHAM Medicago truncatula/Glomus versiforme mixed EST 11brary CDNA clone MHAM-2Pl7, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  /cultivar="Medicago truncatula genotype A17"
/db_xref="taxon:119092"
/clone="MHAM-2P17"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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                                                                                                                                                                                            AW584593.1 GI:7261647
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Percent Similarity: 100.000
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US-09-485-529-104 x AW584593
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seq_name: gb_estl:AW584593
                                                      Quality:
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VERSION
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ORGANISM
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ORIGIN
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FEATURES

TITLE

COMMENT

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/lab_host="E. coli strain XLOLR"

/note="Vector: pBluescript SK-; Site_1: EcoRI; Site_2:
Xhoi; cDNA was prepared from polyA+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
directioncally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."

158 c 118 g 175 t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Length: 17
Gaps: 0
Percent Identity: 94.118
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US-09-485-529-104 x AW584661
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17 a 17

to: 683

from: 1

Align seg 1/1 to: AW584593

VERSION KEYWORDS SOURCE ORGANISM

AUTHORS TITLE

REFERENCE

JOURNAL

COMMENT

DEFINITION

ACCESSION

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/clone_lib="HoGA"
//clone_lib="HoGA"
//clone_lib="HoGA"
//clone_lib="HoGA"
//clone_lib="day old seedling roots"
//dev_stage="24 hours after treatment in the dark at 26 C
with 0.5 mg/ml oligogalacturonides (DP 6-20) in the
presence of 100 ug/ml Gentamicin"
/lab_host="XLOLR"
/note="Yector: PBluescript SK-; Site_l: EcoRI; Site_2:
//note="Yector: PBluescript SK-; Site_l: EcoRI; Site_2:
//note="Yector in PBluescript SK-; Site_l: EcoRI; Site_2: EcoRI; 
                                                                                                                                                                                                                                                                                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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LOCUS BG440209 684 bp mRNA EST 15-MAR-2001
DEFINITION GA__Ea0006G06f Gossypium arboreum 7-10 dpa fiber library Gossypium
EST508687 HOGA Medicago truncatula cDNA clone pHOGA-15H23 5' end
                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 (bases 1 to 748)
Hahh, M.G., Ojanen-Reuhs, T., Samac, D., Town, C.D., Van Aken, S., Utterback, T., Cho, J. and Fraser, C.M.
ESTs from roots of Medicago truncatula treated with oligogalacturonides of DP 6-20
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: hahn@ccrc.uga.edu
G390674e TIGR sequence name: MTMBU40TK More information is
available at: www.medicago.org
available at: www.medicago.org
seq primer: Sknod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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Gaps: 0
Percent Identity: 94.118
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          University of Georgia
220 Riverbend Road, Athens, GA 30602-4712,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /organism="Medicago truncatula"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Unpublished (2001)
Contact: Michael G. Hahn
Complex Carbohydrate Research Center
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: BG647068 from: 1 to: 748
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    /cultivar="A17"
/db_xref="taxon:3880"
/clone="pHOGA-15H23"
                                             mRNA sequence.
BG647068
BG647068.1 GI:13782180
                                                                                                                                                                                                                                                                  Medicago truncatula
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Fax: 706-542-4412
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US-09-485-529-104 x BG647068
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Percent Similarity: 100.000
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COMMENT
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//tissue_trpe="Root hairs & tips"
//dev_stage="2-3 day old seedlings"
//note="Organ: Root; Vector: pBK-CNV; Site_1: ECORI;
//note="Organ: Root; Vector: pBK-CNV; Site_1: ECORI;
//note="Organ: Root; Vector: pBK-CNV; Site_1: ECORI;
//dew_w/w. Short; CDNA was synthesized from a pooled mRNA prep
from elongating root hairs (30% w/w) and 2-3cm root tips
//dew_w/w. xhor-oligo-dT linker-primer and EcoRI;
//dew_w/w. xho
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               truncatula cDNA library
Plant Physiol. 117 (4), 1325-1332 (1998)
Contact: Long SR
Department of Biological Sciences and Howard Hughes Medical
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 (bases 1 to 719)
Covitz, P.A., Smith, L.S. and Long, S.R.
Expressed sequence tags from a root-hair-enriched medicago
                                                                                                                                                                                                                                                                  AA660952 719 bp mRNA EST 08-M
00849 MtRHE Medicago truncatula cDNA 5', mRNA sequence
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       298 GACGAGTTGTTAGCAGCATTAGGTTACAAGGTTCGCTCTTCCGACATGGC 347
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Gaps: 0
Percent Identity: 94.118
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Gilbert Biology, Stanford, CA 94305-5020,
723 3232
Fax: 650 725 8309
Email: fa.srl@forsythe.stanford.edu

    719 "Medicago truncatula" /cultivar="Jemalong"

                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to: AA660952 from: 1 to: 719
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/clone_lib="MtRHE"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 mRNA
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Percent Similarity: 100.000
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US-09-485-529-104 x AA660952
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                                                                                                                              seq_name: gb_estl:AA660952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  barrel medic.
                                                                                                                                                                                                                    seq_documentation_block:
LOCUS AA660952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
LOCUS BG647068
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Institute
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Quality:
                                                                                                                                                                                                                                                                                                                                                   AA660952
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             255
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_scores
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                                        367 T 367
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      17 a 17
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source

FEATURES

BASE COUNT ORIGIN

18

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/organism="Medicago truncatula/Glomus versiforme mixed EST
                                                                                                                                                                                    Email: mjharrison@noble.org
Other name: MHAM-2a-H09; Date: 3/14/00; Updated to the Database of
Expressed Sequence Tags (dbEST) on 04/27/00; More information is
available at 'http://chrysie.tamu.edu/medicago'.
Seq primer: T3.
  ESTs from roots of Medicago truncatula after colonization with
                                                                                                                                                                                                                                                                                                                                                                                      /cultivar="Medicago truncatula genotype Al7"
/db_xref="taxon:119092"
                                                                                                       The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73401
Tel: 580-223-5810
Fax: 580-221-7380
                                                                                                                                                                                                                                                                                                       Location/Qualifiers
1. .712
                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone="MHAM-2017
                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="MHAM"
                                        Unpublished (2000)
Contact: Harrison M.J.
Plant Biology Division
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            AW688657.1 GI:7563393
                      Glomus versiforme
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x AW584431
                                                                                                                                                                                                                                                                                                                                                                        library"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: AW584431
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Percent Similarity: 100.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Medicago.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores
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KEYWORDS
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                                             JOURNAL
                                                                                                                                                                                                                                                                                                         FEATURES
  TITLE
                                                               COMMENT
                                                                                                                                                                                                               Wing, R.A., Frisch, D., Yu, Y., Main, D., Rambo, T., Simmons, J., Henry, D., Wood, T.C., Leslie, A. and Wilkins, T.A.

In integrated analysis of the genetics, development, and evolution of the cotton fiber
Unpublished (2000)
                                                                                                     Gossypium arboreum
Eukaryota: Viridiplantae: Streptophyta: Embryophyta: Tracheophyta;
Spermatophyta: Magnoliophyta: eudicotyledons: core eudicots;
Rosidae: eurosids II; Malvales; Malvaceae: Gossypium.
1 (bases 1 to 684)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /db_xref="taxon:29729"
/clone="GA_Ea0006G06f"
/clone=lib="GASSYpium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Medicago truncatula/Glomus versiforme mixed EST library.
Medicago truncatula/Glomus versiforme mixed EST library
Bukaryota; mixed EST libraries.

1 (bases 1 to 712)
Harrison,M.J., Liu,J., Peng,H., Gonzales,M., Ellis,L., Town,C.D..
Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AW584431 712 bp mRNA w210477e MHAM Medicago truncatula/Glomus versiforme mixed EST library cDNA clone MHAM-2017, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
145 c 138 g 196 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       229 GACGAGTTATTAGCTGTTTTGGGTTACAAAGTTCGGTCATCAGATATGGC 278
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
arboreum cDNA clone GA_Ea0006G06f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 17
Gaps: 0
Percent Identity: 88.235
                                                                                                                                                                                                                                                                                                                         Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Gorden Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /organism="Gossypium arboreum"
/strain="AKA"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      to: 684
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 682.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /lab_host-"E. coli"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /cultivar-"8400"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Email: rwing@clemson.edu
                                          BG440209.1 GI:13349859
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AW584431.1 GI:7261485
                                                                                     Gossypium arboreum.
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US-09-485-529-104 x BG440209
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               74.00
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Ratio:
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                  ACCESSION
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SOURCE
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ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ORGANISM
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KEYWORDS
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                                                                                                                                                                                             REFERENCE
                                                                                                                                                                                                                   AUTHORS
                                                                                                                                                                                                                                                                                                    JOURNAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          AUTHORS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FEATURES
                                                                                                                                                                                                                                                              TITLE
                                                                                                                                                                                                                                                                                                                             COMMENT
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/tissue_type_miner
/tissue_type_miner
/tissue_type_miner
/dev_stage="Roots harvested at 10, 17, 22, 31 and 38 days
post-incollation with Glomus versiforme. The library was
made from a mixture of RNA from each of these stages."
/lab_host="E. coli strain XLOLR"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBluescript SR: site_!: ECORI; Site_2:
Xhot: CDNA was prepared from poly+ enriched RNA from
roots harvested at 10, 17, 22, 31 and 38 days
post-incollation with Glomus versiforme. The CDNA was
directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing CDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Medicago truncatula
Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots,
Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Trifolieae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
LOCUS AW688657 651 bp mRNA EST 15-JUN-2000
DEFINITION NF010B04S71F1000 Developing stem Medicago truncatula cDNA clone
NF010B04S7 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      117 GACGAGTTGTTAACAGCATTAGGTTACAAGGTTCGCTCTTCCGACATGGC 366
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Length: 17
Gaps: 0
Percent Identity: 88.235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: 712
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1
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seq_documentation_block:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                87
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 17 a 17
                                                                                                                                                                                                                                                                                  source
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                                                                                                                                                                                                                                                        FEATURES
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
LOCUS A1495884 311 bp mRNA EST 01-DEC-1999
DEFINITION sb17d07.y1 Gm-c1004 G1ycine max cDNA clone GENOME SYSTEMS CLONE ID:
    Gm-c1004-9062 5' similar to TR:023643 023643 RGA2 PROTEIN. [1] ;,
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Shoemaker, R., Kelin, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, A., Bolla, B., Marra, M., Hillier, L., Kucaba, T., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptoe, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
                     He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                          Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               /tissue_type="stem"
/dev_stage="Pooled developmental"
/dev_stage="Pooled developmental"
/note="vector: Lambda Zap; Contains a mixture of
internodal stem segments"
139 c 143 g 175 t 1 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Contact: Shoemaker R/Public Soybean EST Project
Public Soybean EST Project
Washington University School of Medicine
                                                                                                                                Unpublished (2000)
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 732
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Identity: 93.750
                                                                                                                                                                                                                                                                                                                                                                                                                                      /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF010B04ST"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         /clone_lib="Developing stem"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Gaps:
                                                                                                                                                                                                                                                                                              Email: radixon@noble.org
Insert Length: 651 Std Error: 0.00
Plate: 010 row: B column: 04
Seq primer: TCACACAGGAAACACTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     to: 651
                                                                                                                  Medicago truncatula stem library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Align seg 1/1 to: AW688657 from: 1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x AW688657
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Ratio: 4.500
Percent Similarity: 100.000
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AI495884
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/note="Vector: policies of the property of the
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           University, Flagstaff, Az 86011, Phone: 520-523-1078 (Dr. Paul Keim), 520-523-1372 (Virginia H. Coryell), Fax: 520-523-7500, emall: paul.keim@nau.edu, virginia.coryellFanu.edu" 74 c 88 g 62 t
                                                                                                                                        Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 Fax: (888)
427-3324 or contact: clones@genomesystems.com or
info@genomesystems.com web site: www.genomesystems.com
Seq primer: -40RP from Gibco
High quality sequence stop: 307.
Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
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/clone_lib="Gm-c1004"
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Gaps: 0
Percent Identity: 82.353
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/lab_host="XL10-Gold"
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Washington University School of Medicine,
      Agriculture and Agri-Food Canada
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 153-3, Kisarazu, Chiba 292-0812, Japan
Email: ynakamuékazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
                                                                                                                                                                                                                                                                     Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta, Spermatophyta, Magnoliophyta, eudicotyledons, core eudicots, Rosidae, eurosids I; Fabales, Fabaceae, Papilionoideae, Loteae,
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/organism="Lotus japonicus"
/db_xref="taxon:340s"
/db_xref="taxon:340s"
/db_xref="taxon:340s"
/clone="wML061all_r"
/clone="wML061all_r"
/dev_srege="young plants (two-week old)"
/dev_srege="young plants (two-week old)"
/dov_srege="young                                                                                                                                                                                                                                                                                                                                                               1 (bases 1 to 365)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
Generation of 7137 non-redundant expressed sequence tags from legume. Lotus japonicus
DNA Res. 7 (2), 127-130 (2000)
      23-MAY-2000
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                                  AV409731 Lotus japonicus young plants (two-week old) Lotus japonicus cDNA clone MWL061e11_r 5', mRNA sequence.
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Gene expression in developing soybean seed coats
Unpublished (2000)
Contact: Gijzen M
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Percent Identity: 82.353
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Percent Similarity: 100.000
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Lotus japonicus
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/tissue_tippe="Seed coats"
/tissue_tippe="Seed coats"
/lab_host="E. coli strain XLOLR"
/note="Vector: pBK-CWY, Site_1: EcoRI; Site_2: XhoI; This cond. library was constructed from polyA+ enriched mRNA from green seed coats in mid to late developemental stage, average fresh weight 250 map per seed. Traces of pod and embryo tissue also present. Complementary DNA was synthesized from mRNA using an XhoI-poly(dT)
linker-primer. EcoRI adopters were ligated to the blunt-ended cDNA fragments and the products were digested with XhoI for directional cloning into lambda ZAP Express vector. This lambda library was amphilited once using E. coli host strain XLI Blue MRF'. Inserts were then subcloned by mass excision using Exassist helper phage for conversion into phagemid vector pBK-CWV in E. coli host
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Shoemaker, R. Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Khanna, Shoemaker, R., Keim, P., Vodkin, L., Erpelding, J., Coryell, V., Rhanna, A., Bolla, B., Martin, J., Beck, C., Wylie, T., Underwood, K., Steptco, M., Theising, B., Allen, M., Bowers, Y., Person, B., Swaller, T., Gibbons, M., Pape, D., Harvey, N., Schurk, R., Ritter, E., Kohn, S., Shin, T., Jackson, Y., Cardenas, M., McCann, R., Waterston, R. and Wilson, R.
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Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Phaseoleae;
1391 Sandford Street, London, Ontario, Canada NSV 4T3 Tel: 519 457 1470
Fax: 519 457 3997
Email: 9ijzenm@em.agr.ca.
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Public Soybean EST Project
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/organism="Glycine max"
/cultivar="Harosoy 63"
/db_xref="taxon:3847"
/clone_llb="GmaxSC"
                                                                                                                           Location/Qualifiers
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US-09-485-529-104 x BE659954
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Percent Similarity: 100.000
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Quality:
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    COMMENT
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XhOI; The CDNA library was constructed from mRNA isolated
from degenerating cotyledons of 9-10 day old etholated
seedlings for the cultivar Williams. Complementary DNA was
synthesized from mRNA using a primer consisting of a
poly(dT) sequence with a XhoI restriction site. EcoRI
adapters were ligated to the blunt-ended cDNA fragments
followed by XhoI digestion. The cDNA fragments were
directionally cloned into the EcoRI-XhoI restriction site
of the pBluescript vector. The ligated cDNA fragments
were transformed into DHIOB host cells (GibcoBR). This
library was constructed in the laboratory of Dr. Randy
                                                        Email: est@watson.wustl.edu
This clone is available through: Genome Systems, Inc. 4633 World
Parkway Circle St. Louis, Missouri 63134 For further information
call: (800) 430-0030 or (314) 427-3222 FAX:(888) 919-3324 or (314)
427-3324 or contact: clones@genomesystems.com or
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
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Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
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                                                                                                                                                                                                                                                                                                                                             /tissue_type="Degenerating cotyledons, 9-10 day old etiolated seedling" /lab_host="DH10B"
4444 Forest Park Parkway, Box 8501, St. Louis, MO 63108, USA
                                                                                                                                                                                                                                                       /organism="Glycine max"
/db_xref="taxon:3847"
/clone="GENOME SYSTEMS CLONE ID: Gm-c1069-471"
/clone_llb="Gm-c1069"
                                                                                                                                                                     info@genomesystems.com web site: www.genomesystems.com
High quality sequence stop: 412.
Location/Qualifiers
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Gaps: 0
Percent Identity: 82.353
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US-09-485-529-104 x BF424878
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Ratio: 4.176
Percent Similarity: 100.000
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Lotus japonicus
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LJNEST47e12r Lotus japonicus nodule library 5 and 7 week-old Lotus japonicus cDNA 5', mRNA sequence.
BI419686.1 GI:15190709
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Loteae;
                                                                                                                                                                                                                                                                                                                                                                                 /dev_stage="5 and 7 week-old plants"
//dov_stage="5 and 7 week-old plants"
//note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI;
Site_2: NotI; The library was prepared using mRNA
extracted from nodules of 5 and 7 week-old Lotus plants.
Nodules were induced by, and contained Mesorhizobium
strain R7A."
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Colebatch, G., Freund, S., Trevaskis, B and Udvardi, M.
Lotus japonicus root nodule ESTs: tools for functional genomics
Unpublished (2000)
Contact: Udvardi MK
                                                                                                                                                                                                                                                     /organism="Lotus japonicus"
/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
/clone_lib="Lotus japonicus nodule library 5 and week-old"
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Molecular Plant Nutrition
Max Planck Institute of Molecular Plant Physiology
Max Planck Institute of Molecular Plant Physiology
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
Seq primer: 77
High quality sequence stop: 478.
Location/Qualifiers
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Max Planck Institute of Molecular Plant Physiology
Am Muchlenberg 1, 14476 Golm, Germany
Fax: 49 331 567 8250
Email: udvardi@mpimp-golm.mpg.de
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Gaps: 0
Percent Identity: 82,353
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Location/Qualifiers
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LOCUS BI419686
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/organism="Arabidopsis thaliana"
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US-09-485-529-104 x AW267879
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Fax: 517 353 9334
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Unpublished (1999)
Contact: Carroll P. Vance
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryóta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                            /note="Organ: Nodule; Vector: pSPORT1; Site_1: SalI; Site_2: NotI: The library was prepared using mRNA extracted from nodules of 5 and 7 week-old Lotus plants. Nodules were induced by, and contained Mesorhizobium strain R7A."
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Fax: 651-649-5058
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AW267879 587 bp mRNA EST 07-SEP-2000 EST306157 DSIR Medicago truncatula cDNA clone pDSIR-8K8, mRNA
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More information, including clone ordering, is available at.
http://chrysie.tamu.edu/medicago
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
                         /clone_lib="Lotus japonicus nodule library 5 and 7 week-old"
                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="5 and 7 week-old plants"
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Gaps: 0
Percent Identity: 82,353
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/cultivar="genotype A17"
/db_xref="taxon:3880"
/clone="pDSIR-8K8"
/clone_lib="DSIR"
                                                                                                                                                                                                                                                                                                                                                                                                                          to: 586
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Minnesota EST name:M250388e
/cultivar="Gifu (B-129)"
/db_xref="taxon:34305"
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Medicago truncatula
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US-09-485-529-104 x BI419686
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With Phytophthora medicaginis."

/dev_stage="roots harvested at 10 days post inoculation with Phytophthora medicaginis."

/dab_nost="E. coli strain XLOLR"

/dot="Vector: paluescript SK-; Site_1: EcoRI; Site_2:
XhoI; cDNA was prepared from polyA+ enriched RNA from roots harvested at 10 days post inoculation with Phytophthora medicaginis. The cDNA was directionally ligated into the Uni-ZAP XR vector from Stratagene and packaged using Gigapack III Gold packaging extracts. Plasmids containing cDNA inserts were excised from the recombinant lambda-ZAP phage using Ex-Assist helper phage and propagated in XLOLR cells. Note: EST may be of fungal
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Email: bening@msu.edu
Michigan State University DNA Sequencing Facility Arabidopsis
Biological Resource Center, The Ohio State University, 309 Botany &
Scology Bidg., 1735 Neil Avenue, Columbus, OH 43210 USA, FAX:
6142920603 TEL: 6142929371.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        224 Biochemistry, Michigan State University, East Lansing, MI 48824
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Eukaryota; thallana
Eukaryota; Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Eukaryota; Viridiplantae: Streptophyta; Embryophyta: Tracheophyta;
Espermatophyta: Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases I to 374)
White, J.A., Todd, J., Newman, T., Focks, N., Girke, T., Martinez de
Illarduya, O., Jaworski, J.G., Ohlrogge, J. and Benning, C.
A new set of Arabidopsis expressed sequence tags from developing
seeds. The metabolic pathway from carbohydrates to seed oil
Plant Physiol. 124 (4), 1582-1594 (2000)
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LOCUS BE524828 374 bp mRNA EST 19-MAR-2001
DEFINITION M54G7STW Arabidopsis developing seed Arabidopsis thallana CDNA
clone M54G7 5', mRNA sequence.
'tissue_type="roots infected with Phytophthora
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 GACGAGTIGITAGCAGCATTAGGTTACAAGGTTCTCTTCCGACATGGC 52
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Gaps: 0
Percent Identity: 88.235
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Dept. of Biochemistry & Molecular Biology
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KEYWORDS
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Sperimatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.

1 (bases 1 to 457)
Newman, T., deBrulin, F.J., Green, P., Keegstra, K., Kende, H., McIntosh, L., Ohlrogge, J., Raikhel, N., Somerville, S., Thomashow, M., Retzel, E. and Somerville, C.
Genes galore: a summary of methods for accessing results from large-scale partial sequencing of anonymous Arabidopsis cDNA clones 95148729
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /clone_lib="Lambda-PRL2"
//note="vector: lambda Zip-Lox; Site_1: Sal; Site_2: Not;
Lambda PRL2 is a cDNA library derived from equal
quantities of 4 pools of mRNA. The mRNA sources were 1) 7
                                                                                                                                 /note="Organ: Developing seed; Vector: pBluescript SK-; Site_1: EcoRI; Site_2: XhoII" 88 c 87 g 102 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         T22782 457 bp mRNA EST 06-NOV-1997 4790 Lambda-PRL2 Arabidopsis thaliana cDNA clone 107E8T7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Contact: Thomas Newman MSU-DDE Land Research Laboratory Michigan State University MSU-DOE-PRL, Michigan State University, Plant Biology Bldg., E.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       On Nov 6, 1997 this sequence version replaced gi:932620
                                                                                                                                                                                                                                                                                                                                                                                                                                                 /db_xref="taxon:3702"
/clone="M54G7"
/clone_lib="Arabidopsis developing seed"
/tissue_type="seed"
/dev_stage="5-13 days after flowering"
/lab_host="E.col1"
                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 82.353
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/Strain="var columbia"
/db_xref="taxon:3702"
/clone="107E8T7"
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Email: 22313tcn@ibm.cl.msu.edu
Seq primer: T7 dye primer
Location/Qualifiers
/strain="Columbia"
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US-09-485-529-104 x BE524828
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                                                                                                                                                                                                                                                                                         Ratio: 4.118
Percent Similarity: 100.000
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LOCUS T22782
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SOURCE
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Arabidopsis thallana
Arabidopsis thallana
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids II; Brassicales; Brassicaceae; Arabidopsis.
1 (bases I to 545)
Asamizu,E., Nakamura,Y., Sato,S. and Tabata,S.
A large scale analysis of cDNA in Arabidopsis thaliana: Generation of 12,028 non-redundant expressed sequence tags from normalized and size-selected cDNA libraries
DNA Res. 7, 175-180 (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    The First Laboratory for Plant Gene Research
Kazusa DNA Research Institute
Yana 1532-3, Kisarazu, Chiba 292-0812, Japan
Email: asamizu@kazusa.or.jp, URL:http://www.kazusa.or.jp/en/plant/.
Location/Qualifiers
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              grown roots; 3) staged plants half with 24 hour light cycle, half on 16 hr light, 8 hour dark-rosettes; 4) same plants as 3 but aerial tissue (stems, flowers and siliques. The vector is BRL's lambda Zip-Lox. The cDNA inserts were directionally cloned with Sal-Not arms using oligo dT primed cONA.

86 c 87 g 125 t 18 others
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/note="Vector: pBluescriptII SK-; Site_1: EcoRI; Site_2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:

LOCUS AY526467 545 bp mRNA EST. 01-SEP-2000

DEFINITION AV526467 Arabidopsis thaliana aboveground organs two to six-week old Arabidopsis thaliana cDNA clone AP214e05R 5', mRNA sequence. ACCESSION AV526467 GI:8685995
day germinated etiolated seedlings; 2) tissue culture
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
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Gaps: 0
Percent Identity: 82.353
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/db_xref="taxon:3702"
/clone="AP214e05R"
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Ratio: 4.118
Percent Similarity: 100.000
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US-09-485-529-104 x T22782
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195 GATGAGCTTTTGGCGTTTTGGGTTACAAGGTCAAAACTTCAGACATGGC 244
                                                                                                                          seq_name: gb_est2:BI267918
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                                                                                                                                                                                                                                                                                                                                                                                              BG442853 655 bp mRNA EST 15-MAR-2001 GA_Ea0018120f Gossypium arboreum 7-10 dpa fiber library Gossypium arboreum cDNA clone GA_Ea0018120f, mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Eukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Sosidae; eurosida II; Malvales; Malvaceae; Gossyplum.

1 (bases 1 to 655)
Wing,R.A., Frisch,D., Yu,Y., Main,D., Rambo,T., Simmons,J., Henry,D., Wood,T.C., Leslie,A. and Wilkins,T.A.

No monography and wilkins,T.A.

of the cotton fiber
Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          /clone="GA_EB0018120f"
/clone_lib="Gossypium arboreum 7-10 dpa fiber library"
/tissue_type="Fibers isolated from bolls harvested 7-10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                /jab_host="E. col!"
/note="Vector: pBK-CMV; Site_1: EcoRI; Site_2: XhoI"
188 c 132 g 170 t
                                                                                                                                                                                          188 GATGAGCTTCTTGCTGTTCTTGGCTACAAGGTTCGATCTTCTGAGATGGC 237
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                                                                                                                                                                   1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
  Gaps: 0
Percent Identity: 82.353
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Contact: Wing RA
Clemson University Genomics Institute
Clemson University
100 Jordan Hall, Clemson, SC 29634, USA
Tel: 864 656 7288
Fax: 864 656 4293
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                                                                                                                          to: 545
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Email: rwing@clemson.edu
Seg primer: TAATACGACTCACTATAGGG
High quality sequence stop: 647.
Location/Qualiflers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /db_xref="taxon:29729"
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US-09-485-529-104 x BG442853
                                                                                 US-09-485-529-104 x AV526467
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  Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                          Align seg 1/1 to: AV526467
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Ratio: 4.118
Percent Similarity: 100.000
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                                                            alignment_block
                                                                                                                                                                                                                                                                                         238 T 238
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KEYWORDS
SOURCE
ORGANISM
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ORIGIN
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AUTHORS
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/organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="Ne112E071N"
/clone="Ib="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

were harvested and pooled. 2 others
                                                                                                                                                                                                                                                                                                                                                Medicago.

1 (bases 1 to 227)

Korth,K., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell,C.J., Flores, H.Y., Inman,J.T., Weller,J.W. and May,G.D.

Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
                                                                                                                                                                                                                                                          Eukaryota, Viridiplantae, Streptophyta, Embryophyta, Tracheophyta,
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
seq_documentation_block: 227 bp mRNA EST 18-JUL-2001 LOCUS BI267918 227 bp mRNA DEFINITION NF112E07IN1F1055 Insect herbivory Medicago truncatula cDNA clone NF112E07IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Unpublished (2000)
Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tel: 501 575 5191
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Email: kkorth@comp.uark.edu
Insert Length: 27 Std Error: 0.00
Plate: 112 row: E column: 07
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    to: 227
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BI267918.1 GI:14873367
                                                                                                                                                                                                                                        Medicago truncatula
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US-09-485-529-104 x BI267918
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Percent Similarity: 100.000
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                                                                                                                                                                                                         barrel medic.
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DEFINITION

ACCESSION VERSION KEYWORDS SOURCE

ORGANISM

REFERENCE AUTHORS JOURNAL

COMMENT

TITLE

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/clone_lhb="MtbA"
/clone_lhb="MtbA"
/clone_lhb="MtbA"
/tissue_type="root tips"
/dev_stage="harvested after 3 days of N-starvation"
/dev_stage="harvested after 3 bays of N-starvation"
/note="Vector: pBluescript pSK; Site_1: EcoRI; Site_2:
XhoI; Plants were grown in an aeroponic chamber for 14
days on nitrogen-rich medium followed by 3 days on N-free
medium. RNA was extracted from root tips (1-3 cm). CDNA
was prepared from polyA+ enriched RNA. The cDNA was
directionally ligated into Uni-zapxR vector from
Stratagene and packaged using Giapack Gold packaging
extracts. Plasmids containing cDNA inserts were
mass-excised from phage stocks using ExAssit helper phage
and propagated in SOLR cells. Clone ordering and
sequencing was performed by the Centre National de
Sequencage (Genoscope, Evry, France)."
40 a 69 c 88 g 101 t
                            Medicago truncatula
bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                  Unpublished (2000)

Contact: Genoscope
Genoscope - Centre National de Sequencage
BP 191 91006 EVRY cedex - France
Email: seqref@genoscope.cns.fr, Web : www.genoscope.cns.fr
Contact : Pascal Gamas and Etienne-Pascal Journet, Laboratoire de
Biologie Moleculaire des Relations Plantes-Microorganismes,
CNRS-INRA, BP 27 31326 Castanet-Tolosan Cedex, France (Email:
Mt-est@toulouse.inra.fr Website:
                                                                                                                                                         1 (bases 1 to 398)
Journet, E.P., Crespeau, H., van-Tuinen, D., Gouzy, J., Jaillon, O.,
Journet, E.P., Carreau, V., Chatagnier, O., Kahn, D., Gianinazzi-Pearson
, V. and Gamas, P.
Medicago truncatula ESTs from nitrogen-starved roots
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      BI267177 442 bp mRNA EST 18-JUL-2001
NR102E07IN1F1055 Insect herbivory Medicago truncatula cDNA clone
NF102E07IN 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://sequence.toulouse.inra.fr/Mtruncatula.html)
Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
/cultivar="Jemalong"
/db_xref="taxon:3880"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: AL371416 from: 1 to: 398
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        /clone-"MtBA44A11"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                BI267177.1 GI:14871977
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US-09-485-529-104 x AL371416
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Percent Similarity: 100.000
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LOCUS B1267177
barrel medic.
                                                                                                                                           Medicago.
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JOURNAL
COMMENT
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                                                                                                                                                                                           AUTHORS
                                                                                                                                                                  REFERENCE
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KEYWORDS
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     SOURCE
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Torres-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula leaf library
Unpublished (2000)
On Jul 14, 2000 this sequence version replaced gi:9191308.
                                                                                                                                                                                                                                                          Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Wagnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Paplionoideae; Trifolieae; Medicago.
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                                                   BE317531 288 bp mRNA EST 21-DEC-2000 NF051B06LF1F1045 Developing leaf Medicago truncatula cDNA clone NF051B06LF 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     /clone_lib="Developing leaf"
/tissue_type="leaf"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of very
young, developing, mature and senescing leaves."
34  77  9  70  t
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Email: gdmay@noble.org
Medicago Genome Initiative accession: MGI:S:21598
Insert Length: 766 Std Error: 0.00
Plate: 051 row: B column: 06
Seq primer: TCACACAGGAAACAGCTATGAC.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Fax: 580 221 7331
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Percent Identity: 76.471
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/db_xref="taxon:3880"
/clone="NFO51B06LF"
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                                                                                                                                                               BE317531.2 GI:11961937
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AL371416
AL371416.1 GI:9671169
EST.
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Ratio: 4.000
Percent Similarity: 100.000
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US-09-485-529-104 x BE317531
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                         seq_documentation_block:
LOCUS BE317531
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source

FEATURES

BASE COUNT ORIGIN

DEFINITION

ACCESSION

VERSION KEYWORDS

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Plant Biology Division
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               92 c
                                                                                                                                                                                 Tel: 580 221 7391
Fax: 580 221 7380
Email: gdmay@noble
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Percent Similarity: 100.000
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US-09-485-529-104 x BF634231
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SOURCE
ORGANISM
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  AUTHORS
                                                                                  JOURNAL
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORIGIN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             /organism="Medicago truncatula"
/db.xref="taxon:3880"
/clone="Nerlozo17N"
/clone="Nerlozo17N"
/clone="lb="Insect herbivory"
/tissue_type="local and systemic leaves"
/dev_stage="mature"
/note="Vector: Lambda Zap; Library was produced from fully expanded M. truncatula leaves of plants fed upon by Spodoptera exigua (beet armyworm) for 24 hours. Systemic (undamaged leaves from injured plants) and wounded leaves were harvested and pooled."

54 a 81 c 93 g 112 t 2 others
                                                                                                                    Korth, K., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula insect herbivory library
                                      Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnollophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolleae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Derrel medic.
Medicago truncatula
Bukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Mosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LOCUS BF634231 454 bp mRNA EST 19-DEC-2000
DEFINITION NF084H12DT1F1103 Drought Medicago truncatula cDNA clone NF084H12DT
                                                                                                                                                                                                                                           Contact: Korth K
Dept. of Plant Pathology
University of Arkansas
217 Plant Science Building, Fayetteville, AR 72701, USA
Tal: 501 575 5191
Fax: 501 575 7601
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                        Email: Kkorthecomp.uark.edu
Insert Length: 442 Std Error: 0.00
Plate: 102 row: E column: 07
Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                               Location/Qualifiers
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                       Medicago truncatula
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                                                                                                                                                                                                                                Unpublished (2000)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ⁽⁵⁾, mRNA sequence.
ACCESSION (BF634231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Ratio: 4.000
Percent Similarity: 100.000
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US-09-485-529-104 x BI267177
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barrel medic.
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LOCUS
BF634231
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KEYWORDS
SOURCE
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Torrez-Jerez, I., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W. and May, G.D.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation Unpublished (2000)
Contact: May GD
Contact: May GD
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Perkway, Ardmore, OK 73402, USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta; Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots; Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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( Losses 1 to 470)
He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           /dev_stage="Pooled timepoints"
/note="Vector: Lambda Zap; Contains a mixture of entire
plantlets harvested in a series of days-post-watering
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Expressed Sequence Tags from the Samuel Roberts Noble Foundation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NF039G01ST1F1000 Developing stem Medicago truncatula cDNA clone NF039G01ST 5', mRNA sequence.
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On Apr 14, 2000 this sequence version replaced g1:7566005.
Contact: Dixon RA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              1 others
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              /organism="Medicago truncatula"
/db_xref="taxon:3880"
/clone="NF084H12DT"
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                                                                                                                                                                                                                                                                                                                                gdmay@noble.org
Length: 454 Std Error: 0.00
                                                                                                                                                                                                                                                                                                                                                                  Insert Length: 454 Std Error: 0.0
Plate: 084 row: H column: 12
Seg primer: TCACACAGGAAACAGCTATGAC.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       /clone_lib="Drought"
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Location/Qualifiers
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"Jab_host="E. coli strain XLOLR"

//Jab_host="E. coli strain XLOLR"

//Jab_host="Vector: pBluescript SK -: Site_1: EcoRI; Site_2:

//Note="Wector: pBluescript SK -: Site_1: EcoRI; Site_2:

//Abl: colnA was prepared from polyA+ enriched RNA. The cDNA

was directionally ligated into the Unizap XR vector from

Stratagene and packaged using Gigapack III Gold packaging

extracts. Plasmids containing cDNA inserts were excised

from the recombinant lambda-Zap phage using Ex-assist

helper phage and propagated in XLOLR cells."

9 6 c 106 g 123 t
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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YondenBosch, K., Endre, G., Hur, J., Moore, J., Beremand, P., Ellis, L., Town, C.D., Bowman, C.L., Craven, M.B., Hansen, T.S., Holt, I.E. and Eraser, C.M.
                                                                                                                                                                                                 /tissue_type="Seedling roots"
/dev_stage="24 hours post-inoculation with Sinorhizobium
meliloti"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       seq_documentation_block:
LOCUS BE205231 495 bp mRNA EST 05-SEP-2000
DEFINITION EST397907 KVO Medicago truncatula cDNA clone pKVO-21C7, mRNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ESTs from unincculated seedling roots of Medicago truncatula Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality: 68.00 Length: 17
Ratio: 4.000 Gaps: 0
Percent Similarity: 100.000 Percent Identity: 76.471
  Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualiflers
                                                                      /organism="Medicago truncatula"
/cultivar="genotype A17"
/db_xref="taxon:3880"
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Fax: 409 845 2891
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Tids sequence name:MTGBK16TK
More information is available at.
http://chrysie.tamu.edu/medicago
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             from: 1 to: 482
                                                                                                                                                    /clone="pKV1-2B16"
/clone_lib="KV1"
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Texas A&M University
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US-09-485-529-104 x BE202661
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KEYWORDS
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Rakaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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AndenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ESTs from roots of Medicago truncatula 24 hours after inoculation with Sinochizobium meliloti Unpublished (1999)
Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               07-SEP-2000
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EST402683 KV1 Medicago truncatula cDNA clone pKV1-2B16, mRNA
                                                                                                                                                                                                                                                /organism="Medicago truncatula"
//db_xref="taxon:3880"
/db_xref="taxon:3880"
/clone="NF0396015T"
/clone=lib="beveloping stem"
/tissue_type="stem"
/dev_stage="Pooled developmental"
/note="Vector: Lambda Zap; Contains a mixture of internodal stem segments"
198 c 98 g 123 t
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               The Samuel Roberts Noble Foundation 2510 Sam Noble Parkway, Ardmore, OK 73402, USA Tel: 580 221 7302 Fats: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 17
Gaps: 0
Percent Identity: 76.471
                                                                                                   Email: radixon@noble.org
Insert Length: 678 Std Error: 0.00
Plate: 039 row: G column: 01
Seg primer: TCACACAGGAAACAGCTATGAC.
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Texas A&M University
College Station, TX 77843-3258, USA
TEL: 409 845 7707
Fax: 409 845 2891
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Texas A&M University:T262354e
TIGR sequence name:MTIAD08TK
                                                                                                                                                                                                      Location/Qualifiers
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     BE202661
BE202661.1 GI:8745925
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US-09-485-529-104 x AW691269
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Ratio:
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28

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Contact: Paiva NL

Plant Biology Division

The Samuel Roberts Noble Foundation

2510 Sam Noble Parkway, Ardmore, OK 73402, USA

Tel: 580 221 7317

Fax: 580 221 7380

Email: nlpaiva@noble.org

Insert Length: 544 Std Error: 0.00

Plate: 018 row: F column: 10

Seq primer: TCACACAGGAAACAGCTATGAC.
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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/db_xref="taxon:3880"
/clone="pKV0-21B13"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NF018F10NR 5', mRNA sequence.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         to: BE205387 from: 1
                                                                                                                                                                                                                              /clone_lib="KV0"
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AW684591.1 GI:7559327
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US-09-485-529-104 x BE205387
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Percent Similarity: 100.000
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LOCUS AW684591
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                                                                                    /organism="Medicago truncatula"
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/clone="taxon:3880"
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Sinorhizobium meliloti (0 hour)"
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/lab_host="E.coli strain XLOLR"
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DBluescript SK -; Site_1: DBluescr
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Medicago truncatula
bukaryota, Viidiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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vandenBosch,K., Endre,G., Hur,J., Moore,J., Beremand,P., Ellis,L.,
Town,C.D., Bowman,C.L., Craven,M.B., Hansen,T.S., Holt,I.E. and
Fraser,C.M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 BE205387 522 bp mRNA EST 05-SEP-2000
EST398063 KVO Medicago truncatula cDNA clone pKVO-21B13, mRNA
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 76.471
Seq primer: SKmod (CTA gAA CTA gtg gAT CC).
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            College Station, TX 77843-3258, USA
Tel: 409 845 7707
Fax: 409 845 2891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               More information is available at. .
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Texas A&M University name:T265159e
TIGR sequence name:MTGBM07TK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              http://chrysie.tamu.edu/medicago
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Contact: VandenBosch K
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            BE205387
BE205387.1 GI:8748684
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Texas A&M University
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Percent Similarity: 100.000
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US-09-485-529-104 x BE205231
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                              FEATURES
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/Lissue_trpe="Seedling roots"
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Sinorhizobium mellioti (0 hour)"
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/lab_host-"E.coli strain XLOLR
was directionally ligated into the Unizap XR vector from
Stratagene and packaged using Gigapack III Gold packaging
extracts. Plasmids containing cDNA inserts were excised
from the recombinant lambda-Zap phage using Ex-assist
helper phage and propagated in XLOLR cells."
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Watson,B.S., Shin,H.-S., Lopez-Meyer,M., Scott,A.D., Harris,A.R.,
Gonzales,R.A., Bell,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May
G.D. and Palva,N.L.
Expressed Sequence Tags from the Samuel Roberts Noble Foundation
Wedicago truncatula nodulated root library
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Medicago truncatula
bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
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Align seg 1/1 to: AW693047
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SOURCE
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Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                       /clone_lib="Nodulated root"
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/dev_stage="rooled developmental"
/note="vector: Lambda Zap; Four-week old Rhizobium
mellioti-inoculated Medicago truncatula roots,
a mixture of young and old roots and nodules."
a mixture of young and old roots and nodules."
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Medicago.

1 (bases 1 to 601)

2 (bases 1 to 601)

2 (bases 1 to 601)

3 (bases 1 to 601)

4 (bases 1 to 601)

5 (bases 1 to 601)

6 (bases 1 to 601)

7 (bases 1 to 601)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Medicago truncatula stem library
Unpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7567783.
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Gaps: 0
Percent Identity: 76.471
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               EST
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/db_xref="taxon:3880"
/clone="NF018F10NR"
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/db_xref="taxon:3880"
/clone="NF059C03ST"
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Email: radixon@oble.org
Insert Length: 653 Std Error: 0.00
Plate: 059 row: C column: 03
Seq primer: TCACAGGAAACAGCTATGAC.
Location/Qualifiers
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                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 544
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cocation/Qualifiers
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Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
Medicago.
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Bell
,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             AW697328 613 bp mRNA EST 21-DEC-2000 NF115E11ST1F1086 Developing stem Medicago truncatula cDNA clone NF115E11ST 5', mRNA sequence.
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L Onpublished (2000)
On Apr 14, 2000 this sequence version replaced gi:7572090.
Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 730
Fax: 580 221 7380
Email: radixon@noble.org
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1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                     38 GATGAACTCTTAGCTGTAGTTGGTTACAAAGTGAAATCTTCAGACATGGC 87
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US-09-485-529-104 x AW690601
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Bukaryota, Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoideae; Trifolieae;
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     He, X.-Z., Shadle, G., Scott, A.D., Harris, A.R., Gonzales, R.A., Bell, C.J., Flores, H.R., Inman, J.T., Weller, J.W., May, G.D. and Dixon
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                                                                                                                                                                                                                                                                                                                                                             AW690574 614 bp mRNA EST 15-JUN-2000 NF031C08ST1F1000 Developing stem Medicago truncatula cDNA clone NF031C08ST 5', mRNA sequence.
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                                                                                                                                                                  5 others
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Contact: Dixon RA
Plant Biology Division
The Samuel Roberts Noble Foundation
2510 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7380
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 17
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US-09-485-529-104 x AW690574
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REFERENCE AUTHORS

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Darrel medic.
Medicago truncatula
Eukaryota; Viridiplantae; Streptophyta; Embryophyta; Tracheophyta;
Spermatophyta; Magnoliophyta; eudicotyledons; core eudicots;
Rosidae; eurosids I; Fabales; Fabaceae; Papilionoldeae; Trifolleae,
                                                                                                                                                                                                                                                                                                                                                                                                                                                       Expressed Sequence Tags from the Samuel Roberts Noble Foundation Medicago truncatula stem library Unpublished (2000) On Apr 14, 2000 this sequence version replaced g1:7565337, Contact: Dixon RA
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He,X.-Z., Shadle,G., Scott,A.D., Harris,A.R., Gonzales,R.A., Be,C.J., Flores,H.R., Inman,J.T., Weller,J.W., May,G.D. and Dixon
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The Samuel Roberts Noble Foundation
The Samuel Roberts Noble Foundation
210 Sam Noble Parkway, Ardmore, OK 73402, USA
Tel: 580 221 7302
Fax: 580 221 7302
Email: radixon@noble.org
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                                               |
| 617.71<br>639.97<br>1675.69<br>1713.16<br>1713.16<br>1713.16<br>1728.01<br>728.01<br>835.15<br>835.15<br>971.26<br>971.26                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | $\begin{smallmatrix} 1 & 1 & 1 & 1 & 1 & 1 & 1 & 2 & 2 & 2 &$                                                           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4.16+03<br>4.16+03<br>4.26+03<br>4.26+03<br>4.26+03<br>4.26+03<br>4.26+03<br>4.46+03                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     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| 100.28<br>100.06<br>199.16<br>99.16<br>99.16<br>99.16<br>00 99.00<br>99.00<br>97.14<br>97.14                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 | 0022                                                                                                                    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85.35<br>85.35<br>85.35<br>86.35<br>84.94                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                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| .seq:US-08-506-553C-7 - seq:US-08-235-836C-35 + seq:US-08-506-553C-22 - seq:US-08-459-967-9 + seq:US-08-460-327-9 + seq:US-08-460-327-9 + seq:US-08-460-327-9 + seq:US-09-328-111-695 + seq:US-09-328-111-695 + seq:US-09-328-111-695 + seq:US-09-388-355A-9 + seq:US-09-087-194-34 + seq:US-09-188-955A-9 + seq:US-09-188-955A-9 + seq:US-09-188-955A-9 + seq:US-09-188-955A-9 + sex. seq:S512660-1 + 32.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 103-09-004-9108-1.4 103-09-004-9108-1.4 103-09-004-9108-1.4 103-08-476-910-3 103-08-476-910-3 103-08-476-910-3 103-08-476-910-3 103-08-476-910-3 103-08-476-910-3 103-08-476-910-3 103-08-476-910-1 103-08-476-910-1 103-08-476-910-1 103-08-476-910-1 103-08-486-6738-6 103-08-910-62-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9112-4 103-08-910-9113-6 103-08-910-913-6 103-08-910-913-6 103-08-910-913-6 103-08-910-913-91-91-91-91-91-91-91-91-91-91-91-91-91-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | /cgn2_6/prodate/2/lna/5A_COMB.seq:US-0/-9//-434-111 + /cgn2_6/prodate/2/lna/5A_COMB.seq:US-08-458-819-111 + /cgn2_6/prodate/2/lna/5A_COMB.seq:US-08-434-255-11 + /cgn2_6/prodate/2/lna/5A_COMB.seq:US-08-434-255-1 + /cgn2_6/prodate/2/lna/5A_COMB.seq:US-08-4459-967-1 + /cgn2_6/prodata/2/lna/5A_COMB.seq:US-08-460-327-1 + /cgn2_6/prodata/2/lna/5A_COMB.seq:US-08-460-327-1 + /cgn2_6/prodata/2/lna/5A_COMB.seq:US-08-459-871-1 + /cgn2_6/prodata/2/lna/5A_COMB.seq:US-08-459-871-1 + /cgn2_6/prodata/2/lna/5A_COMB.seq:US-07-671-817A-2 + /cgn2_6/prodata/2/lna/5A_COMB.seq:US-08-460-327-1 + /cgn2_6/prodata/2/lna/5A_COMB.seq:US-08-46 |

| gn2_6/ptodata/2/ina/5B_COMB.seq:US-08-754-282B-5 - 32.00 84 gn2_6/ptodata/2/ina/5A_COMB.seq:US-07-671-817A-1 + 32.00 84 gn2_6/ptodata/2/ina/5A_COMB.seq:US-08-149-100-1 + 32.00 84. gn2_6/ptodata/2/ina/5A_COMB.seq:US-07-671-817A-3 + 32.00 84.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | .7e+03<br>.8e+03<br>8e+03<br>.9e+03      | 2940<br>2990<br>1024<br>3066 |
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| Z_0/ptodata/Z/Ina/SA_COMB.seq:US-08-453-104-23 + 32.00 83<br>2_6/ptodata/Z/ina/SB_COMB.seq:US-08-694-824-23 + 32.00 83<br>2_6/ptodata/Z/ina/SR_COMB.seq:US-08-453-104-22 + 32.00 83                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  | 5.2e+03<br>5.2e+03<br>5.2e+03            | 3200<br>3200<br>3201         |
| gn2_6/ptodata/2/ina/5B_COMB.seq:US-08-694-824-22 + 32.00 83<br>gn2_6/ptodata/2/ina/5A_COMB.seq:US-08-006-676B-2 + 32.00 83                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 5.2e+03<br>5.5e+03                       | 3201<br>3319                 |
| Pptcdatd/lna/5A_COMB.seq:US-08-282-845-1 + 32.00 83.<br>Pptcdata/2/lna/5B_COMB.seq:US-08-428-414A-4 + 32.00 83.<br>Pptcdata/2/lna/PpCTUS COMB.seq:PCT-US94-00324-2 + 32.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 5.5e+03<br>5.5e+03<br>30 5.5e+03         | 319<br>3319<br>33            |
| gn2_6/ptodata/2/ina/5A_COMB.seq.US-08-349-867-18 + 32.00 82<br>gn2_6/ptodata/2/ina/5A_COMB.seq.US-08-239-476-18 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 5.8e+03<br>5.8e+03                       | 3465<br>3465                 |
| gn2_6/ptodata/2/ina/5A_COMB.seq:US-08-598-305A-18 + 32.00 8<br>qn2_6/ptodata/2/ina/5B_COMB.seq:US-08-639-923A-18 + 32.00 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 5.8e+03                                  | 3465<br>3465                 |
| n2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US95-05431-18 + 32.00<br>n2_6/ptodata/2/ina/5A_COMB.seq:US-07-951-715A-1 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 3.87 5.8e+(<br>5.8e+03                   | 34                           |
| gn2_6/ptodata/2/ina/5B_COMB.seq:US-08-459-448A-1 + 32.00 82<br>gn2_6/ptodata/2/ina/6A_COMB.seq:US-08-459-595A-1 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 5.8e+03<br>5.8e+03                       | 34                           |
| n2_6/ptodata/2/ina/6A_COMB.seq:US-08-459-504B-1 + 32.00<br>n2_6/ptodata/2/ina/6A_COMB.seq:US-08-459-444-1 + 32.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    | 5.8e+03                                  | 34                           |
| 2_6/ptodata/2/ina/5A_COMB.seq:US-08-530-492-164 + 32.00 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 5.8e+03                                  | w «                          |
| 2_6/ptodata/2/ina/5A_COMB.seq.US-07-828-788A-7 + 32.00 82<br>5 6/ptodata/2/ina/5A_COMB.seq.US-07-828-788A-7 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 5.9e+03                                  | 330                          |
| 2_6/ptodata/2/ina/PCIUS_COMB.seq:PCT-US92-11337-7 + 32.00<br>5.6/ptodata/2/ina/PCIUS_COMB.seq:PCT-US92-11337-7 + 32.00<br>6.6/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/2/ina/ptodata/ | 8 5.9e+0.                                | )                            |
| 2 6/ptodata/2/ina/6A_COMB.seq:US-08-754-490-27 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 5.9e+03                                  | 35                           |
| 2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-27 + 32.00 8<br>2_6/ptodata/2/ina/6A_COMB.seq:US-08-922-505A-33 + 32.00 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 67 5.9e+03<br>67 5.9e+03                 | ຕຕ                           |
| 2_6/ptodata/2/ina/6B_COMB.seq:US-09-260-952A-27 + 32.00 8<br>2_6/ptodata/2/ina/6B_COMB.seq:US-09-253-341-27 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | .67 5.9e+03                              | നഗ                           |
| 2_6/ptodata/2/ina/02_comp.seq:US-09-253-341-33 + 32.00 82<br>2_6/ptodata/2/ina/6E_COMP.seq:US-09-253-341-33 + 32.00 82<br>3_6/rt-data-2/jina/6E_COMP.seq:US-09-253-331a-77 + 32.00                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   | 57 5.9e+03                               | 3534                         |
| 2_6/ptodata/2/ina/6E_COMB.seq.US-09-253-331A-33 + 32.00 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 5.9e+03                                  | າຕູ                          |
| /ptcdata/2/ina/5A_COMB.seq:US-U8-3/7-690-3 + 32.00 82.<br>/ptcdata/2/ina/5B_COMB.seq:US-08-713-815A-2 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 5.96+03 3<br>6 6.06+03                   | ກຕ                           |
| 2_6/ptodata/2/ina/5A_COMB.seq:US-08-602-737-7 + 32.00 82.<br>2_6/ptodata/2/ina/6A_COMB.seq:US-08-754-490-29 + 32.00 82                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | .0e+03<br>6.0e+03                        | 35                           |
| 2_6/ptodata/2/lna/6A_COMB.seq:US-08-922-505A-29 + 32.00 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 6.0e+03                                  | ט ג                          |
| Z_6/ptodata/2/ina/6B_COMB.seq:US-09-260-952A-29 + 32.00 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 54 6.0e+03                               | <u> </u>                     |
| ptodata/2/ina/6B_COMB.seq:US-09-253-341-29 + 32.00 82<br>ptodata/2/ina/6B_COMB.seq:US-09-253-331A-29 + 32.00 8                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 6.0e+03<br>6.0e+03                       | ຕ                            |
| 2_6/ptodata/2/ina/6A_COMB.seq:US-08-936-135-5 - 32.00 82.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | .2e+03                                   | 52                           |
| 2_6/ptodata/2/im/5_COMB.seq:US-08-735-893-1 + 32.00 81.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | .8e+03                                   | 996                          |
| Z_0/ptodata/2/ina/3A_COMB.Seq4:05-06-446-466-1 + 3Z.00 01.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | . 9e+03                                  | 55                           |
| Z_6/ptodata/z/ina/backfiles1.seq:5254/99-3 + 32.00 80.94<br>2_6/ptodata/2/ina/5A_COMB.seq:US-08-377-690-2 + 32.00 80.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                | .7e+03                                   | 34                           |
| 2_6/ptodata/2/ina/5A_COMB.seq:US-08-486-380-1 + 32.00 80.<br>2_6/ptodata/2/ina/5B_COMB.seq:US-08-436-080-1 + 32.00 80.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | .7e+03<br>.7e+03                         | 36                           |
| gn2_6/ptodata/2/ina/5B_COMB.seq:US-08-250-848-1 + 32.00 80.<br>gn2_6/ptodata/2/ina/5B_COMB.seq:US-08-438-192-1 + 32.00 80.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 7.7e+03 4.7.7e+03 4.3                    | 36                           |
| 2_6/ptodata/2/ina/5B_COMB.seq:US-08-475-971-1 + 32.00 80.<br>2_6/ptodata/2/ina/6A_COMB.seq:US-09-021-203-1 + 32.00 80.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | .7e+03<br>.7e+03                         | 36                           |
| gn2_6/ptodata/2/lna/5B_COMB.seq:US-08-754-282B-6 - 32.00 80                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 7.7e+03                                  | ω 4                          |
| 912_6/ptodata/2/ina/6B_COMB.seq:US-09-175-828-72 + 32.00 80                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | 7.9e+03                                  | 44                           |
| gnz_o/ptodata/z/ina/5b_COMB.seq:US-08-631-097-3 + 32.00 799.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | 9.0e+03 4                                | 900                          |
| 2_6/ptodata/2/lna/5A_COMB.seq:US-U8-766-014-1 + 32.00 78.<br>2_6/ptodata/2/lna/6B_COMB.seq:US-08-456-200B-5 + 32.00 78                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 1.0e+04                                  | 5.4                          |
| ghz_b/ptodatd//ina/Ab_COMB.seq:uS-08-810-112-9 + 31.00 //.<br>gpn2_6/ptodatd//ina/6A_COMB.seq:uS-08-675-566.5 - 32.00 77.<br>mn 6/t-data-1/7/in/6A_COMB.seq:uS-08-675-566.5 - 32.00 77.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              | . 2e+04                                  | ກດາດ                         |
| gn2_6/ptodatd///ina/6A_COMB.seq:US-08-6/5-586-14 32.00 76.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1 1 3e+04 6                              | 200                          |
| gnz_b/ptcdata/z/ina/bb_cOMB.seq:US-U8-9/5-70z-46 + 3z.UU /3<br>gnz_b/ptcdata/z/ina/bb_cOMB.seq:US-09-295-028-46 + 3z.UO 75<br>m2                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | ./1 1.4e+04<br>.71 1.4e+04<br>71 1.4e+04 | 7091<br>7091<br>7091         |
| 2_6/ptodata/2/ina/6B_COMB.seq:US-09-381-862-4 + 32.00 75.                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            | 1.4e+04 7                                | ) <del>-+</del>              |

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| ് 4 പപര്ദ്ധധധധധധധ വധധ സസ നസ നെയയ                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       | 962<br>963<br>963<br>963<br>963                                                                                                                                                                                                                                                                                                |
| 1.56+04<br>1.66+04<br>1.86+04<br>1.88+04<br>1.88+04<br>1.88+04<br>2.06+04<br>2.06+04<br>3.56+04<br>3.56+04<br>3.56+04<br>3.56+04<br>1.06+05<br>3.56+04<br>1.06+05<br>3.56+04<br>1.06+05<br>3.56+04<br>1.06+05<br>3.56+04<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+05<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+03<br>1.106+                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             | 1.4e+03<br>1.4e+03<br>1.4e+03<br>1.4e+03<br>1.4e+03                                                                                                                                                                                                                                                                            |
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| 88 - 748 - 54<br>88 - 748 - 54<br>89 - 248 - 54<br>89 - 248 - 17<br>89 - 248 - 24<br>89 - 24 | 08-097-5<br>08-480-6<br>08-295-8<br>08-488-3                                                                                                                                                                                                                                                                                            |
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| 2505<br>2505<br>2505<br>2505<br>2505<br>2505<br>2506<br>2506                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           | 1185<br>1185<br>1215<br>1215                                                                                                                                                                                                                                                                                                            |
| 1. 8e+03                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               | 2.3e+03 1185<br>.4e+03 1215<br>.4e+03 1215                                                                                                                                                                                                                                                                                              |
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| 553-167 + 31.50                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | 168.3 + 31.00 89.86 2.4e+03 1185<br>108177-2 + 31.00 89.76 2.4e+03 1185<br>638.1 + 31.00 89.61 2.4e+03 1215<br>36-17 + 31.00 89.61 2.4e+03 1215                                                                                                                                                                                         |
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| 553-167 + 31.50                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | US-08-954-916A-3 + 31.00 89.86 2.4e+03 1185<br>GY-08-31-916A-3 + 31.00 89.86 2.4e+03 1185<br>GY-08-242-663A-1 + 31.00 89.61 2.4e+03 1215<br>US-08-954-536-17 + 31.00 89.61 2.4e+03 1215                                                                                                                                                 |
| 553-167 + 31.50                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        | US-08-954-916A-3 + 31.00 89.86 2.4e+03 1185<br>GY-08-31-916A-3 + 31.00 89.86 2.4e+03 1185<br>GY-08-242-663A-1 + 31.00 89.61 2.4e+03 1215<br>US-08-954-536-17 + 31.00 89.61 2.4e+03 1215                                                                                                                                                 |
| \$\text{SECOMB}\$ \text{Seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{55.} \text{Comb}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{55.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2556 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ 84-105-105-105-105-105-105-105-105-105-105                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | Amb.seq:161.0537.05303.0 31.00 89.86 2.4e+03 1185 8eq:105-08-1916A-3 + 31.00 89.86 2.4e+03 1185 8eq:105-08-1916A-3 + 31.00 89.61 2.4e+03 1215 8eq:105-08-954-536-17 + 31.00 89.61 2.4e+03 1215                                                                                                                                          |
| \$\text{SECOMB}\$ \text{Seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{55.} \text{Comb}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{55.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-653-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2555 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ \text{84-24}\$ 4 \text{86-03}\$ 2556 \\ \text{64.} \text{Comp}\$ \text{seq: 105-06-757-63-167}\$ + \text{31-50}\$ 84-105-105-105-105-105-105-105-105-105-105                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      | // ina/fa_COMB.seq:US-08-31-916A-3 + 31.00 89.86 2.4e+03 1185<br>/2/ina/Fa_COMB.seq:US-08-31-916A-3 + 31.00 89.86 2.4e+03 1185<br>/2/ina/PCTUS_COMB.seq:PCT-US91-08177-2 + 31.00 89.76 2.4e+03 1187<br>/2/ina/fa_COMB.seq:US-08-242-663A-1 + 31.00 89.61 2.4e+03 1215<br>/2/ina/fa_COMB.seq:US-08-954-536-17 + 31.00 89.61 2.4e+03 1215 |
| 6. Proclate 22/1na/5B_COMB. seq: US-00-757-653-167         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-757-653-189         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-757-653-189         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-757-653-189         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-757-653-189         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-757-653-189         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-759-519-118         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-759-314-118         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-759-314-118         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-759-314-118         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-759-314-118         31.50         84.24         4.88+13         2505           6. Proclate 22/1na/5B_COMB. seq: US-00-759-                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          | prodate/2/ina/Fice_Coms.seq:US-08-391-916A-3 + 31.00 89.86 2.4e+03 1185<br>/ptodate/2/ina/FB_COMB.seq:US-08-391-916A-3 + 31.00 89.86 2.4e+03 1185<br>/ptodate/2/ina/FCTUS_COMB.seq:US-08-242-663A-1 + 31.00 89.6 2.4e+03 1215<br>/ptodate/2/ina/6A_COMB.seq:US-08-954-536-17 + 31.00 89.61 2.4e+03 1215                                 |

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| 299-14 + 4                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             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| LCOMB. seq: PCT-US93-00324-29  While seq: US-08-185-282-10 + 34  While seq: US-08-185-282-11 + 34  While seq: US-08-185-282-11 + 34  While seq: US-08-185-282-11 + 34  While seq: US-08-18-282-11 + 34  While seq: US-09-178-252-1 - 34  While seq: US-09-178-252-1 - 34  While seq: US-09-178-252-1 - 34  While seq: US-08-18-19-18  While seq: US-09-233-336A-20  While seq: US-09-232-200-66 + 34  While seq: US-09-232-197-66 + 34  While seq: US-09-232-197-67  While seq: US-09-232-336-7-37  While seq: US-09-232-336-7-37  While seq: US-09-402-036-7-37  While seq: US-08-484-101B-49  While seq: US-08-484-101B-49  While seq: US-08-832-832-837  While seq: US-08-832-837-837  While seq: US-08-832-837-837-837  While seq: US-08-832-837-837-837-837-837-837-837-837-837-837                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     | 88B-37 + 88B                                                                                                                                                                                                                                                                                                                                                                                                                                                                    |
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| 7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+04<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03<br>7e+03 |
| \$6 7.7e+03 2493 \$8.0.56 7.7e+03 2493 \$8.0.56 7.7e+03 2496 \$5.57 7.7e+03 2502 \$5.57 7.7e+0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| \$6 7.7e+03 2493 \$8.0.56 7.7e+03 2493 \$8.0.56 7.7e+03 2496 \$5.57 7.7e+03 2502 \$5.57 7.7e+0                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| 30.50         80.56         7.7e+03         2493           30.50         80.56         7.7e+03         2496           30.50         80.55         7.7e+03         2502           30.50         80.55         7.7e+03         2502           30.50         80.52         7.7e+03         2502           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50         80.52         7.7e+03         2504           30.50 </td                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          |
| coda to 2/1/10a/5A_COMB. seq:105-07-977-441-5+ 30.50 80.56 7.77e+03 2493 coda to 2/1/10a/5A_COMB. seq:105-07-977-441-5+ 30.50 80.56 7.77e+03 2493 coda to 2/1/10a/5A_COMB seq:105-01438-619-5 30.50 80.56 7.77e+03 2493 coda to 2/1/10a/5A_COMB seq:105-01438-29-5 30.50 80.56 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-01431-29-5 30.50 80.55 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-01431-29-2 30.50 80.55 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-01431-29-2 30.50 80.55 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-01431-29-2 30.50 80.55 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-0141-29-2 30.50 80.55 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-014-20-2 30.50 80.55 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-014-20-2 30.50 80.55 7.77e+03 2495 coda to 2/1/10a/5A_COMB seq:105-014-2 30.50 80.55 7.77e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.50 80.52 7.77e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.50 80.52 7.77e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.40-7 4 30.50 80.52 7.7e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.40-7 4 30.50 80.52 7.7e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.50 80.52 7.7e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.40-7 4 30.50 80.52 7.7e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.50 80.52 7.7e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.50 80.52 7.7e+03 2502 coda to 2/1/10a/5A_COMB seq:105-014-2 30.50 80.52 7.7e+03 2502 coda to 2/10a/5A_COM                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            |

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ATTORNEY/AGENT INFORMATION
            COMPUTER READABLE FORM:
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COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      US-08-981-256A-4
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1137
         1074
                                                                                                                                                                                                                                                                                                     /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-096-181A-11 + 30.00 87.11 3.3e+03
/cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US94-08326-11 + 30.00 87.11 3.3e+03
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-347-819-5 + 30.00 86.72 3.5e+03 11
/cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-346-11 - 30.00 86.62 3.6e+03 11
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-346-883-2 - 30.00 86.59 3.6e+03 11
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-172-339-3 - 30.00 86.59 3.6e+03 11
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-172-339-3 - 30.00 86.59 3.6e+03 11
/cgn2_6/ptodata/2/ina/5B_COMB.seq:US-09-120-211-10 - 30.00 86.59 3.6e+03 11
/cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-189-256A-10 - 30.00 86.54 3.6e+03 11
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-189-256A-10 - 30.00 86.54 3.6e+03 11
/cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-189-18826-9 + 30.00 86.54 3.6e+03 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICANT: Meinhard HASSLACHER et al. TITLE OF INVENTION: (S)-HYDROXY-NITRILE-LYASE FROM HEVEA BRASILIENSIS NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAl 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-08-981-256A-4
                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Gaps: 0
Percent Identity: 82.353
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-09-117-853-1 from: 1 to: 1964
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: Wenderoth, Lind & Ponack, L.L.P. STREET: 2033 K Street, N.W., Suite 800 CITY: Washington
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM: Arabidopsis thaliana US-09-117-853-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Ratio: 4.118
Percent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       1 0.S.A.
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TYPE: DNA
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seq_documentation_block:

Sequence 5, Application US/07916901

Patent No. 5364772

GENERAL INCOMMATION:

APPLICANT: Granneman, James G.

APPLICANT: Lahners, Kristine N.

APPLICANT: Rao, Donald D.

TITLE OF INVENTION: e @3.ADRENERGIC RECEPTOR PROTEIN AND DNA

TITLE OF INVENTION: E @3.ADRENERGIC RECEPTOR PROTEIN AND DNA

TITLE OF INVENTION: E G3.ADRENERGIC RECEPTOR PROTEIN AND DNA

CORRESPONDENCES: 9

CORRESPONDENCES: 9

ADDRESSEE: REISING, ETHINGTON, BARNARD, PERRY &

ADDRESSEE: MILTON

ADDRESSEE: MILTON
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ADDRESSEE: MILTON
STREET: 201 W. Big Beaver - Ste. 400; P.O. Box 4390
CITY: Troy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-07-916-901-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   116 CTCCTTGAGGCACTTGGCCACAAGGTTACTGCACTGGACCTTGCA 160
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3 LeuLeualaalaLeuGlyTyrLysValargalaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 66.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: US-08-981-256A-4 from: 1 to: 1078
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: PatentIn Release #1.0, Version #1.25
     Diskette, 3.5 inch, 1.44 mb
MEDIUM TYPE: Diskette, 3.5 inch, 1.44
COMPUTER: IDM Competible
OPERATING SYSTEM: MS-DOS
SOFTWARE: Wordperfect 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/981,256A
FILING DATE: December 22, 1997
CLASSIFICATION: 435
PRIOR APPLICATION GATA:
APPLICATION NUMBER:
FILING DATE:
FILING DATE:
                                                                                                                                                                                                                                                                                                                                   NAME: Matthew Jacob
REGISTRATION NUMBER: 25,154
REFERENCE/DOCKET NUMBER: 1553-021112
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 721-8200
TELEFAX: (202) 721-820
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICATION NUMBER: US/07/916,901
FILING DATE: 19920720
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 48099
COMPUTER REAABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x US-08-981-256A-4
                                                                                                                                                                                                                                                                                                               ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 1078 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           45.00
3.750
80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       nucleic acid
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COUNTRY:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Michael E.
TITLE OF INVATION: No. 5476781el Entomopoxvirus Expression System
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               to: 2005
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-991-867B-43
                                                                                                                                                                                                                                                                                                                                                                                                         Length: 13
Gaps: 0
Percent Identity: 76.923
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to reverse of: US-07-916-901-5 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC-1992
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             130 GTGTTGGCTGCACTGGGTCCCAAGGTGGGGGCGTCTGAC 92
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
NAME: Kohn, Kenneth I.
REGISTRATION NUMBER: 30,955
REFERENCE/DOCKET NUMBER: P-324 (WSU)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (313) 689-3554
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 2005 base pairs
TYPE: NUCLEIC ACID
STRANDEDNESS: SINGle
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    PRICE APPLICATION DATA:
APPLICATION NUMBER: WO 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME: Saliwanchik, David R.
REGISTRATION NUMBER: 31.794
REFERENCE/DOORET NUMBER: UF114.C3
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-485-529-104 x US-07-916-901-5/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
; Sequence 43, Application US/07991867B
; Detent No. 54767B1
; GENERAL INFORMATION:
                                                                                                                                                                                                                                     CDNA to mRNA
                                                                                                                                                                                                                                                                                                                                                                                                       42.00
3.818
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 32606
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                               CDS
51..1250
                                                                                                                                                                                                                  linear
                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       USA
                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                               Ratio:
                                                                                                                                                                                                                  TOPOLOGY: 11:
MOLECULE TYPE:
                                                                                                                                                                                                                                                                           NAME/KEY:

LOCATION:
US-07-916-901-5
                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CITY: (
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APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5476781el Entomopoxvirus Expression System
NUMBER OF SEQUENCES: 66
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-991-867B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-DEC 1992
CLASSIFICATION NUMBER: US/07/991,867B
FILING APPLICATION DATA:
APPLICATION NUMBER: US/07/991,867B
FILING DATE: 12-FEB-1992
PROOR APPLICATION NUMBER: US/07/827,685
FILING DATE: 30-JAN-1992
PROOR APPLICATION NUMBER: US/07/827,685
FILING DATE: 30-JAN-1992
PROOR APPLICATION NUMBER: US/07/657,584
FILING DATE: 19-FEB-1991
ATFORNEY/AGENT INFORMATION:
NAME: SA11*MANCHIK, DAVIG R.
REGISTRATION NUMBER: 31,794
REFERENCE/DOCKET NUMBER: 31,794
REFERENCE/DOCKET NUMBER: UF-14.C3
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
TELECOMMULICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-07-991-867B-43 from: 1 to: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: David R. Saliwanchik
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  eq_documentation_block:
Sequence 45, Application US/07991867B
Batent No. 54/6781
GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x US-07-991-867B-43
                                                                                                                                                                           ; MOLECULE TYPE: DNA (genomic)
US-07-991-8678-43
TELEFAX: 904-372-5800
INPORMATION FOR SEQ ID NO: 4
SEQUENCE CHARACTERISTICS:
LENGTH: 235 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TELEFAX: 904-372-5800 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                           3.727
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          32606
                                                                                                                                                                                                                                                                                                   Quality:
Ratio:
Percent Similarity:
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alignment_block:
US-09-485-529-104 x US-08-544-332-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TELECOMMUNICATION INFORMATION: TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               45:
                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-544-332-43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     REFERENCE/DOCKET NUMBER:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bencen, Gerard H. REGISTRATION NUMBER: 35
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 235 base pairs TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                           41.00
3.727
78.571
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        904-372-5800
single
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              USA
                                                                                                                                                              Percent Similarity:
STRANDEDNESS:
                                                                                                                           Quality:
                                                                                                                                              Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32606
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STATE: FL
COUNTRY: U
                                                                                                            alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
CORRESPONDENCES: 77
                                                                                                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-544-332-43
                                                                                                                                                                                                                                                                                                                  Percent Identity: 64.286
                                                                                                                                                                                                                                                         Align seg 1/1 to: US-07-991-867B-45 from: 1 to: 235
                                                                                                                                                                                                                                                                                            2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/544,332
                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRICE APPLICATION: 433
PRICE APPLICATION DATA:
APPLICATION NUMBER: US 07/991,867
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/107,755
FILING DATE: 19-AUG-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: W0 92/14818
FILING DATE: 12-FEB-1992
PRIOR APPLICATION NUMBER: W0 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION NUMBER: US 07/857,584
FILING DATE: 19-FEB-1991
ATTORNEY,AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     UF114.C4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
BEDIOM TYPE: Floppy disk
CMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x US-07-991-867B-45
                                                                                                                                                                                                                                                                                                                                                                                                 REGISTRATION NUMBER: 35,746
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 REFERENCE/DOCKET NUMBER: UF
TELECOMMUNICATION INFORMATION:
TELEPHONE: 904-375-8100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      TELEFAX: 904-372-5800
INFORMATION FOR SEQ ID NO: 43:
SEQUENCE CHARACTERISTICS:
                 ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-07-991-867B-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 NAME: Bencen, Gerard H.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                LENGTH: 235 base pairs
TYPE: nucleic acid
                                                                                                                                                3.727
78.571
                                                                                                                             41.00
single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            USA
STRANDEDNESS:
                                                                                                                                                            Percent Similarity:
                                                                                                                           Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               32606
                                                                                                          alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              COUNTRY:
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APPLICANT: Moyer, Richard W.
APPLICANT: Hall, Richard L.
APPLICANT: Hall, Richard L.
APPLICANT: Gruidl, Michael E.
TITLE OF INVENTION: No. 5935777el Entomopoxvirus Expression System
WINBER OF SEQUENCES: 77
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-544-332-45
                      Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                     SOFTWARE: PATENTIN FELGASE #1.0, Version #1.25
CURRENT APPLICATION DATA:
FILING DATE:
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION DATA:
FILING DATE: 07-DEC-1992
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
                                                                                                                                                                       Align seg 1/1 to: US-08-544-332-43 from: 1 to: 235
Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE: Gerard H. Bencen
STREET: 2421 N.W. 41st Street, Suite A-1
CITY: Gainesville
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/827,685
FILING DATE: 30-JAN-1992
PRIOR APPLICATION DATA:
APPLICATION UNBER: US 07/657,584
FILING DATE: 19-FEB-1991
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   US 08/107,755
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 APPLICATION NUMBER: US 08/107,75 FILING DATE: 19-AUG-1993 APPLICATION DATA: APPLICATION NUMBER: WO 92/14818 FILING DATE: 12-FEB-1992
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alignment\_scores

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q_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-424-224-1
                                                                                                                                                                                                                                                                                                                                                84 GAATTATTGAACGTCAAAGGTTATCTGTTAAAGCATCCGAT 125
                                                                                                                                                              Gaps: 0
Percent Identity: 64.286
                                                                                                                                                                                                                                                                                                                         2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                 lign seg 1/1 to: US-08-544-332-45 from: 1 to: 235
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     CDNA AND
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ZIP: 10134
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/424,224
FILLING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/ACENT INCRMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          REFERENCE/DOCKET NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-758-4800
TELEFAX: 212-751-6849
TELEFX: 421792
INFORMATION FOR SEQ ID NO: 1: SEQUENCE CHARACTERISTICS: LENGTH: 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                               Sequence 1, Application US/08424224
Patent No. 512173
GENERAL INFORMATION:
TITLE OF INVENTION: USES THEREOF
TITLE OF INVENTION: USES THEREOF
                                                                                                                                                                                                                       ignment_block:
S-09|485-529-104 x US-08-544-332-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: UNKNOWN
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUMBER OF SEQUENCES: 2
CORRESPONDENCE ADDRESS:
ADDRESSEE: MORGAN & FINNEGAN
STREET: 345 PARK AVE.
                    TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
08-544-332-45
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ORGANISM: MURINE
; INDIVIDUAL ISOLATE: IL-2R
US-08-424-224-1
                                                                                                                                                              3.727
78.571
                                                                                                                                       41.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
  single
                                                                                                                                                                                                                                                                                                                                                                                                                                                  g_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NEW YORK
NEW YORK
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ANTI-SENSE: NO ORIGINAL SOURCE:
STRANDEDNESS:
                                                                                                                       ignment_scores:
Quality:
                                                                                                                                                              Ratio:
                                                                                                                                                                               ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STATE:
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seq_documentation_block:

Sequence 64, Application PC/TUS9402891

Sequence 65, Application PC/TUS9402891

Sequence 64, Application PC/TUS9402891

Sequence 64, Application PC/TUS9402891

Sequence 64, Application PC/TUS9402891

APPLICANT: THE GOVERNMENT OF THE UNITED STATES OF AMERICA AS

APPLICANT: REPRESENTED BY THE SECRETARY, DEPARTMENT OF HEALTH AND HUMAN

APPLICANT: SERVICES

APPLICANT: SERVICES

APPLICANT: OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

TITLE OF INVENTION: METHODS FOR DIAGNOSIS AND TREATMENT OF

STATES: MORGAN & FINNEGAN

STREET: 345 PARK AVE.

CITY: NEW YORK

STATE: NEW YORK

STATE: NEW YORK
                                                                                                                                                                   to: 1608
Length: 13
Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-424-224-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: WORD PERFECT # 5.1
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US94/02891
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PRIOR APPLICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/031,143
FILING DATE: 12-MAR-1993
APPLICATION NUMBER: 08/121,435
FILING DATE: 14-SEPT-1993
ATTORNEY/AGENT INFORMATION:
NAME: WILLIAM S. FEILER
REGISTRATION NUMBER: 26,728
REFERENCE/DOCKET NUMBER: 2026-406
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFAX: 212-758-4800
                                                                                               alignment_block:
US-09-485-529-104 x US-08-424-224-1/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: FLOPPY DISK
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; INDIVIDUAL ISOLATE: IL-2R
PCT-US94-02891-68
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEX: 421792
INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS: LENGTH: 1608
41.00
3.727
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: NUCLEIC ACID
STRANDEDNESS: SINGLE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             ZIP: 10154
COMPUTER READABLE FORM:
MEDIUM TYPE: FLOPPY
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: UNKNOWN
                          Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              ANTI-SENSE:
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alignment\_scores:

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28234
       alignment_scores
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Fatent No. 6140486

GENERAL INFORMATION:
FAPLICANT: Calgene, LLC

TITLE OF INVENTION:
TITLE OF INVENTION: Of POLYMetide-like synthesis genes in plants
TITLE OF INVENTION: Of POLYMetide-like synthesis genes in plants
TITLE OF INVENTION: Of POLYMetide-like synthesis genes in plants
TITLE OF INVENTION: Of POLYMetide-like synthesis genes in plants
CURRENT APPLICATION NUMBER: US/09/090, 793

CURRENT FILING DATE: 1998-06-04

EARLIER PILING DATE: 1997-06-04

NUMBER OF SEQ ID NOS: 66

SEQ ID NO 12

LENGTH: 40138
                                                                                                                                                                                                                                                                                                                                                  seq_documentation_block:
    Sequence 13, Application US/09090793
    Patent No. 6140486
    GENERAL INFORMATION:
    APPLICANT: Calgene, LLC
    TITLE OF INVENTION: Production of polyunsaturated fatty acids by expr.
    TITLE OF INVENTION: of polykeide-like synthesis genes in plants
    FILE REPERBNCE: CROE.131.0105
    CURRENT APPLICATION NUMBER: US/09/090,793
    CURRENT FILING DATE: 1998-06-04
    BARLIER FILING DATE: 1997-06-04
    NUMBER OF SEQ ID NOS: 66
    SOFTWARE: PatentIn Ver. 2.0
    SEQ ID NO 13

                                                                                                                                                                         Align seg 1/1 to reverse of: PCT-US94-02891-68 from: 1 to: 1608
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to reverse of: US-09-090-793-13 from: 1 to: 19227
                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/1na/6A_COMB.seq:US-09-090-793-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/6A_COMB.seq:US-09-090-793-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Length: 10
Gaps: 0
Percent Identity: 80.000
                                Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                    13732 GAACTGATACTTGCGCTTGGGTATAAAGTC 13703
                                                                                                                         US-09-485-529-104 x PCT-US94-02891-68/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   2 GluLeuLeuAlaAlaLeuGlyTyrLysVal 11
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-485-529-104 x US-09-090-793-13/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            40.00
4.444
90.000
41.00
3.727
84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ORGANISM: Vibrio marinus
US-09-090-793-13
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                ; ORGANISM: Vibrio marinus US-09-090-793-12
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Quality:
Ratio:
                                                  Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Similarity:
                           Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           19227
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_scores:
                                                                                                       alignment_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TYPE: DNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TYPE: DNA
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GENERAL INFORMATION:
APPLICANT: Manmias, Clara
APPLICANT: Benorine, Jean L.
APPLICANT: Strosbergic Denny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
CITY: Charlotte
STATE: No. 5691155th Carolina
COUNTRY: USA
                                                                                                                                                             to: 40138
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 298
                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-7
                                                                                                                                                             Align seg 1/1 to reverse of: US-09-090-793-12 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to reverse of: US-08-087-772A-7 from: 1
                            Gaps: 0
Percent Identity: 80.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: DA PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              81 GTGTTGGCTGCACTGGGGTCCAGGGTAGGGGCGCGTCCGAC 43
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length:
                                                                                                                                                                                                                                    30715 GAACTGATACTTGCGCTTGGGTATAAAGTC 30686
                                                                                                                                                                                                          2 GluLeuLeuAlaAlaLeuGlyTyrLysVal 11
                                                                                           alignment_block:
US-09-485-529-104 x US-09-090-793-12/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_block:
US-09-485-529-104 x US-08-087-772A-7/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3339-195
                                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
; Sequence 7, Application US/08087772A
; Patent No. 5691155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3335;
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEFAN: 919-881-3175
INFORMATION FOR SEQ ID NO: 7:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        26,419
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; MOLECULE TYPE: DNA (genomic) US-08-087-772A-7
40.00
4.444
90.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 298 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3.545
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                                               Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
       Quality:
                            Ratio:
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Sequence 4, Application US/08087772A
Sequence 4, Application US/08087772A
Patent No. 5691155
GENERAL INFORMATION:
APPLICANT: Nahmias, Clara
APPLICANT: Emorine, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
            GENERAL INFORMATION:
APPLICANT: Nabmias, Clara
APPLICANT: Mannias, Jean L.
APPLICANT: Strosberg, Donny A.
TITLE OF INVENTION: Nucleotide Sequences Encoding the Murine
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Length: 13
Gaps: 0
Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to reverse of: US-08-087-772A-3 from:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            ADDRESSEE: Bell, Seltzer, Park & Gibson STREET: Post Office Drawer 34009 CITY: Charlotte STATE: No. 5691155th Carolina
                                                                                                                                                                                                                 ADDRESSEE: Bell, Seltzer, Park & Gibson
STREET: Post Office Drawer 34009
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-485-529-104 x US-08-087-772A-3/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3339-195
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE:
CLASSIFICATION: 800
ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond O.
REGISTRATION NUMBER: 26,419
REFRENCE/DOCKET NUMBER: 3339-
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
TELEPHONE: 919-881-3175
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                              STREET: Post CITY: Charlotte
STATE: No. 5691155th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1164 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 nucleic acid
EDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            84.615
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               US-08-087-772A-3
                                                                                                                                                                                                                                                                                                          TITLE OF INVENTION: COMPOSITION FOR THE DETECTION OF GENES ENCODING TITLE OF INVENTION: RECEPTORS AND PROTEINS ASSOCIATED WITH CELL PROLIFERATION WIMBER OF SEQUENCES: 134
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q_name: /cgn2_6/ptodata/2/1na/5A_COMB.seq:US-08-087-772A-3
q_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-276-531-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MEDIUM TYPE: Floppy disk COMPUTER: IBM PC COMPATIBLE OPERATING SYSTEM: PC-DOS/MS-DOS SOFTWARE: Word Perfect 6.1 for Windows/MS-DOS 6.2 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 70.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 703
                                                                                                                                                                                                                                                                                                                                                                                                             E: INCYTE PHARMACEUTICALS, INC 3174 PORTER DRIVE
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            lign seg 1/1 to: US-09-276-531-31 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PA-0008 US
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            1 AspGluLeuLeuAlaAlaLeuGlyTyrLys 10
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        APPLICATION NUMBER: US/09/276,531
FILING DATE: Herewith
CLASSIFICATION:
                                                                                                            GENERAL INFORMATION:
APPLICANT: Bandman, Olga
APPLICANT: Lal, Preeti
APPLICANT: Hillman, Jennifer L.
APPLICANT: Yue, Henry
APPLICANT: Reddy, Roopa
APPLICANT: Beddy, Roopa
APPLICANT: Baughn, Mariah R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            q_documentation_block:
Sequence 3, Application US/08087772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PRIOR APPLICATION DATA:
APPLICATION NUMBER: 60/079,677
FILING DATE: March 27, 1998
CLASSIFICATION:
                                                                 Sequence 31, Application US/09276531
Patent No. 6183968
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ATORNEY AGENT INFORMATION:
NAME: Lynn E Murry, Ph.D.
REGISTATION UNDRER: 42,918
REFERENCE/DOCKET NUMBER: PA-OF
TELECOMMUNICATION INFORMATION:
TELEPHONE: (650) 855-0555
TELEFAX: (650) 855-4166
INFORMATION FOR SEQ ID NO: 31:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ignment_block:
is-09-485-529-104 x US-09-276-531-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 703 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Ratio: 3.900 ercent Similarity: 100.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM: | MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          PROSTUT01
                                                                                                                                                                                                                                                                                                                                                                                                                                                             PALO ALTO
CALIFORNIA
                                             [_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 94304
                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ignmėnt_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  6-531-31
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                           STREET:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE:
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TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-881-3140
                                                                                                                                                                                                                                                                                                                                                                          Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FILING DATE
                                                                                                                                                                                                                                       ; NAME/KEY:
; LOCATION:
US-08-087-772A-1
                                                                                                                                                                                                                                                                                                                                                      alignment_scores
                                                                                                                                                                                                                     FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICANT: Emorine, Jean L.
APPLICANT: Emorine, Jean L.
APPLICANT: Excoberg, Donny A.
TITLE OF INVENTION: Beta3-Adrenergic Receptor and Their Applications
NUMBER OF SEQUENCES:
ADDRESSE: Bell, Seltzer, Park & Gibson
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                g_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-087-772A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    lign seg 1/1 to reverse of: US-08-087-772A-4 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 69.231
                                                                                                   SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA: APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              SOFTWARE: Patentin Release #1.0, Version #1.30 CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/087,772A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Bell, Seltzer, Park & Gibson STREET: Post Office Drawer 34009 CITY: Charlotte CITY: No 5691155th Carolina COUNTRY: USA
                                                                                                                                                                      FILING DATE:
CLASSIFICATION: 800
ATTONNEY/AGENT INFORMATION:
NAME: LINKET, RAYMOND 0.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
TELECHOME: 919-881-3140
TELEFAX: 919-881-3175
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ignment_block:
S-09-485-529-104 x US-08-087-772A-4/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       ATTORNEY/AGENT INFORMATION:
NAME: Linker, Raymond 0.
REGISTRATION NUMBER: 26,419
REFERENCE/DOCKET NUMBER: 3339-195
                           COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOCTWARE: PatentIn Release
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release *1 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         q_documentation_block:
Sequence 1, Application US/08087772A
Patent No. 5691155
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                               INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS: LENGTH: 1360 base pairs TYPE: nucleic acid STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.545
84.615
                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        CLASSIFICATION: 800
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      FILING DATE:
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to: 1920
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
    Sequence 3 Application Us/08450962
    Patent No. 6274706
    Patent No. 6274706
    Sequence 3 Papelication Us/08450962
    Patent No. 6274706
    APPLICANT: EMORINE, Laurent; MARULLO, Stefano;
    TITLE OF INVENTION: GENES
    NUMBER OF SEQUENCES: 9
    CORRESPONDENCE ADDRESS: ADDRESSE: RECK, MAHIN & CATE
    STREET: P.O. BOX 06110
    CITY: CHICAGO
    STATE: ILLINOIS
    COMPRY: US.A.
    COMPRY: US.A.
    COMPUTER READABLE FORM:
    MEDIUM TYPE: 3-1.72 diskette
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to reverse of: US-08-087-772A-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            CLASSIFICATION: 530
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/117,829
FILING DATE: 08-SEPT-1993
APPLICATION NUMBER: 07/721,571
FILING DATE: 25-MAY-1990
PRIOR APPLICATION NUMBER: PCT/FR89/00918
FILING DATE: 25-JAN-1989
ATTORNEY/AGENT INFORMATION:
NAME: Fleit, Martin; Gollin, Michael REGISTRATION NUMBER: 16,900; 31,957
REFERENCE/DOCKET NUMBER: 47078-042
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                              Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x US-08-087-772A-1/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/450,962
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 E: 3-1/2" diskette
IBM compatible
                                                                                                                                                                                     TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TELEPHONE: (202) 789-3400
TELEFAX: (202) 789-1158
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM compatible OPERATING SYSTEM: MS-DOS SOFTWARE: ASCII
TELEPHONE: 919-881-3140
TELEFAX: 919-881-3175
INFORMATION FOR SEG ID NO: 1
SEQUENCE CHARACTERISTICS:
LENGTH: 1920 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                        39.00
3.545
84.615
                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                   CDS
568..1731
                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Percent Similarity:
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to: 1491

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374 GAGACTTTGCTGAAAAGATATGGGTACCGGATACGTTCTTCGCCAATG 421
                                                                              1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-768-301-1
                                       Align seg 1/1 to: US-08-137-614A-3 from: 1
US-09-485-529-104 x US-08-137-614A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                               RY: U.S.A.
10112-0228
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               MOLECULE TYPE: CI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         FRAGMENT TYPE:

ORIGINAL SOURCE:
US-08-768-301-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     GENERAL INFORMATION:
APPLICANT: Soderlund, David M.
APPLICANT: Knipple, Douglas C.
APPLICANT: Henderson, Joseph E.
TITLE OF INVENTION: Gene Encoding An Insect
TITLE OF INVENTION: Gamma-Aminobutyric Acid (GABA) Receptor Subunit NUMBER OF SEQUENCES: 31
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                     to: 3437
                                                                                                                                                                                                                                                                                                                                                                                                                                       q_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-137-614A-3
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/137,614A
FILING DATE: 15-OCT-1993
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                     lign seg 1/1 to reverse of: US-08-450-962-3 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 43.750
                                                                                                                                                                                                                     Percent Identity: 69.231
                                                                                                                                                                                                                                                                                                                                                                               3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  E: Nixon, Hargrave, Devans & Doyle Clinton Square, P.O. Box 1051
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ATTORNEY/AGENT INFORMATION:
NAME: Tinian, Susan J.
REGISTRATION NUMBER: 34,103
REFERENCE/POCKET NUMBER: 19603/120
TELECOMMUNICATION INFORMATION:
TELEPHONE: (716)263-1636
TELEFRAX: (716)263-1600
INFORMATION FOR SEQ ID NO: 3:
                                                                                                                                                                                                                                                           ignment_block:
S-09-485-529-104 x US-08-450-962-3/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                             q_documentation_block:
Sequence 3, Application US/08137614A
Patent No. 5487976
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
        LENGTH: 343/ LLENGTH: TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      38.00
3.455
68.750
                                                                                                                                                                          39.00
3.545
84.615
SEQUENCE CHARACTERISTICS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STREET: Clinton
CITY: Rochester
STATE: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
                                                                                                                                                                              Quality:
Ratio:
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                                                                                                                                                                                                                 ercent Similarity:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TOPOLOGY: 11
MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        int_scores:
                                                                            TOPOLOGY:
                                                                                                                                                             gnment_scores
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seq_documentation_block:
    Sequence 1, Application US/08768301
    Patent No. 5854002
    GENERAL INFORMATION:
    APPLICANT: Tomalski, Michael D.
    APPLICANT: Gant, Daniel B.
    TITLE OF INVENTION: METHOD OF IDENTIFYING COMPOUNDS THAT BIND TITLE OF EQUENCES: 6
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                    ADDRESSEE: Brumbaugh, Graves, Donohue & Raymond STREET: 30 Rockefeller Plaza CITY: New York
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Gaps: 0
Percent Identity: 43.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            to: 1491
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Align seg 1/1 to: US-08-768-301-1 from: 1
                                                                                                                                                                                                                                                                                                                                                                               MEDIUM TYPE: Diskette
COMPUTER: IBM Compatible
OPERATING SYSTEM: DOS
SOFTWARE: FastSEQ Version 1.5
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/768,301
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  A30693
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ATTORNEY/AGENT INFORMATION:
NAME: MacLeod, Janet M
REGISTRATION UNMBER: 35,263
REFRENCE/CDCKET NUMBER: A306!
TELECOMMUNICATION INFORMATION:
TELEPHONE: 212-408-2500
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-485-529-104 x US-08-768-301-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              INFORMATION FOR SEQ ID NO: 1:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SEQUENCE CHARACTERISTICS:
LENGTH: 1491 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               38.00
3.455
68.750
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: 212-765-2519
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER:
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12936..13487

LOCATION:

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seq_documentation_block:
    Sequence 14, Application US/08799464A
    Sequence 14, Application US/08799464A
    Patent No. 2998601
    GENERAL INFORMATION:
    APPLICANT: Murtaugh, Michael P. et al.
    TITLE OF INVENTION: WETHODS OF USE
    TITLE OF INVENTION: METHODS OF USE
    NUMBER OF SEQUENCES: 35
    CORRESPONDENCE ADDRESS:
seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-799-464A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/799,464A
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME/KEY: misc_feature
LOCATION: 212.7402
LOCATION: 212.77402
OTHER INFORMATION: /citation= "LV ORF 1a"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  NAME/KEY: misc_feature
'LOCATION: 12394..13191
OTHER INFORMATION: /citation= "LV ORF 3"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: misc_feature
|LOCATION: 11786..12535
|UNIVER INFORMATION: /standard_name="LV ORF 2"
| OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     OD: experimental /evidence= EXPERIMENTAL
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ADDRESSEE: John M. Collins
STREET: 2405 Grand Blvd., Suite 400
CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            /label= ORF1b
/citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CLASSIFICATION: 536
PRIOR APPLICATION DATA:
APPLICATION NUMBER: 08/287,941
FILING DATE: August 5, 1994
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 26,262
REFERRUCE/DOCKET NUMBER: 22907
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ZIP: 64108
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            TELEPHONE: (816) 474-9050
TELEFAX: (816) 474-9057
INFORMATION FOR SEQ 1D NO: 14:
SEQUENCE CHARACTERISTICS:
LENGTH: 15101 base pairs
TYPE: nucleic acid
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         | NAME/KEY: misc_feature | LOCATION: 7384..11775 | LIDENTIFICATION METHOD: GOTHER INFORMATION: /label OTHER INFORMATION: /
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ORGANISM: Arteriviridae STRAIN: VR-2332
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        NAME/KEY: misc_feature
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MOLECULE TYPE: CDNA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         unknown
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     HYPOTHETICAL: NO ANTI-SENSE: NO ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  FEATURE:
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    Sequence 14, Application PC/TUS9509927
    GENERAL INFORMATION:
    APPLICATION: Wachael P.
    TITLE OF INVENTION: WR-12332 VIRAL NUCLEOTIDE SEQUENCE AND TITLE OF INVENTION: METHODS OF USE NUMBER OF SEQUENCES: 26
    CORRESPONDENCE ADDRESS:
    ADDRESSEE: John M. Collins STREET: 1101 Walnut, Suite 1400
    CITY: Kansas City
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              9088 GACCGCATCCTGCTCTTGCATATCACATGAAGGCGCAGAAC 9132
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ; RELEVANT RESIDUES IN SEQ ID NO: 14: FROM 1 TO 15101
US-08-799-464A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Moormann, R. J.
Lelystad virus, the causative agent of
procine epidemic abnortion and respiratory
syndrome (PEARS) is related to LDV and EAV
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Gaps: 0
Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PatentIn Release #1.0, Version #1.25
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                                                                                                       "LV ORF 5"
                                                                                                                                                                                                                                                                                                                           "LV ORF 7"
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Align seg 1/1 to: US-08-799-464A-14 from: 1
                                                                                     LOCATION: 13484..14089
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LOCATION: 14588..14974
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PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CUUMAAA.

COMPUTER READABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM PC compatible

COMPUTER: PC PC POSS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_block:
US-09-485-529-104 x US-08-799-464A-14
                                                                                                                                                                                                                                                                                                                                                                                              Meulenberg, J. J.M.
                                                                                                                                                                                                                                                                                                                                                                                                                Hulst, M. M.
de Veijer, E. J.
Moonen, P. L.
den Besten, A.
de Kluyver, E. P.
Wensvoort, G.
                                                               NAME/KEY: misc_feature
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93.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Virology
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          CITY: Kansas Cit
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SOFTWARE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TITLE: SI
JOURNAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS:
AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                              AUTHORS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    AUTHORS
                                                                                                                                                    FEATURE:
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NAME/KEY: misc_feature
LOCATION: 212.7402
LOCATION: 212.77402
NFB INFORMATION: /standard_name= "LV ORF la"
OTHER INFORMATION: /citation= ([1])
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OTHER INFORMATION: /evidence= EXPERIMENTAL
OTHER INFORMATION: /label= ORF1b
OTHER INFORMATION: /citation= ([1])
FEATURE:
NAME/KE: misc_feature
LOCATION: 11786..12535
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LOCATION: 14588..14974
CHER INFORMATION: /standard_name= "LV ORF 7"
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      •
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LOCATION: 14077.14598
OCHER INFORMATION: /citation= "LV ORF
OTHER INFORMATION: /citation= ([1])
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: misc_feature
LOCATION: 13484..14089
OTHER INFORMATION: /standard_name= "LV ORF
OTHER INFORMATION: /citation= ([1])
            APPLICATION NUMBER: PCT/US95/09927
FILING DATE:
CLASSIPLATION:
ATTORNEY/AGENT INFORMATION:
NAME: COllins, John M.
REGISTRATION NUMBER: 2297
REFERENCE/DOCKET NUMBER: 2297
TELECOMMUNICATION INFORMATION:
TELEPHONE: (816) 474-9050
TELEPHONE: (816) 474-9057
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
LENGHH: 15101 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TOPOLOGY: unknown
MOLECULE TYPE: cDNA
HYPOTHETICAL: NO
AMTI-SENSE: NO
ORIGINAL SOURCE:
ORGANISM: Arteriviridae
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Meulenberg, J. J.M.
Hulst, M. M.
de Veijer, E. J.
Moonen, P. L.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            den Besten, A.
de Kluyver, E. P.
Wensvoort, G.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: misc_feature
LOCATION: 7384..11775
IDENTIFICATION METHOD:
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      PUBLICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   AUTHORS:
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Seguence 1, Application US/08157005

Seguence 1, Application US/08157005

Sequence 1, Application US/08157005

Setent No. 5620691

GENERAL INFORMATION:

APPLICANT: Wenervoort, Gert

APPLICANT: Moorman, Robertus J

APPLICANT: Meulenberg, Johannes M

APPLICANT: Meulenberg, Johannes M

APPLICANT: Meulenberg, Johannes M

APPLICANT: Meulenberg, Johannes M

TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS

NUMBER OF SEGUENCES:

ADDRESSEE: Cooper & Dunham

STREET: 30 Rockefeller Plaza

COUNTY: New York

STATE: New York

COUNTY: New York

STATE: New York
AUTHORS: Moormann, R. J.

TITLE: Lelystad virus, the causative agent of
TITLE: procine epidemic abnortion and respiratory
TITLE: syndrome (PEARS) is related to LDV and EAV.
JOURNAL: Virology
VOLUME: 192
PAGES: 62-72
PAGES: 62-72
BATE: 1937
RELEVANT RESIDUES IN SEQ ID NO: 14: FROM 1 TO 15101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-157-005-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 1 AspGluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Align seg 1/1 to: PCT-US95-09927-14 from: 1 to: 15101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Gaps: 0
Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.24
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/157,005
FILING DATE: 26-NOV-1993
CLASSIFICATION: 424
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRIOR APPLICATION NUMBER: EP 92200781.0
FILING DATE: 18-MAR-1992
PRIOR PAPLICATION NUMBER: EP 92200781.0
FILING DATE: 05-JUN-1992
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
APPLICATION NUMBER: PCT/NL92/NUMBER: APPLICATION NUMBER: PCT/NL92/NUMBER: PCT/NUMBER: PCT/NUMBER: PCT/NUMBER: PCT/NUMBER: PCT/NUMBER: PCT/NUMBER: P
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REGISTRATION NUMBER: 16,579
REFERENCE/DOCKET NUMBER: 44819
TELECOMMUNICATION INFORMATION:
TELEPHONE: (212) 977-9550
TELEFAX: (212) 315-1931
TELEFAX: 422523 COOP UI
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x PCT-US95-09927-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                2.714 93.333
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MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    10112
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Salt Lake City
                      STATE: Ut
COUNTRY:
ZIP: 8411
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Pa_documentation_block:
Sequence 1, Application US/08747863
Patent No. 6197310
GENERAL INFORMATION:
GENERAL INFORMATION:
APPLICANT: Wensvoort, Gert
APPLICANT: Pol, Johannes
APPLICANT: Pol, Johannes
APPLICANT: Meulenberg, Johanna J
TITLE OF INVENTION: CAUSITIVE AGENT OF THE MYSTERY SWINE DISEASE,
TITLE OF INVENTION: VACCINE COMPOSITIONS AND DIAGNOSTIC KITS
NUMBER OF SEQUENCES: 9
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-747-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    38.00 Length: 15
2.714 Gaps: 0
93.333 Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             lign seg 1/1 to: US-08-157-005-1 from: 1 to: 15108
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Trask, Britt & Rossa
STREET: 525 South 300 East
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  1gnment_block:
S-09-485-529-104 x US-08-157-005-1
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INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15108 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 11786..12532
OTHER INFORMATION:
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 14077..14595
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                               NAME/KEY: CDS
LOCATION: 12394..13188
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         NAME/KEY: CDS
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-08-157-005-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NAME/KEY: CDS
LOCATION: 12936..13484
OTHER INFORMATION:
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LOCATION: 7384..11772
OTHER INFORMATION:
                                                                                                                                                           NAME/KEY: CDS
LOCATION: 212..7399
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   lignment_scores:
Quality:
`Ratio:
Percent Similarity:
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FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/157,005
FILING DATE: 26-NOV-1993
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 91201398.4
FILING DATE: 06-JUN-1991
PRIOR APPLICATION DATA:
APPLICATION NUMBER: EP 9200781.0
FILING DATE: 18-MAR-1992
PRIOR APPLICATION DATA:
APPLICATION NUMBER: PCT/NL92/00096
FILING DATE: 05-JUN-1992
ATOCNEY AGENT INFORMATION:
NAME: TUNING: Allen C.
REGISTRATION NUMBER: 33041
REFERENCE/DOCKET NUMBER:
TELECOMMUNICATION INFORMATION:
TELEPHONE: (801) 531-9168
INFORMATION FOR SED ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 15108 base pairs
TYPE: nucleic acid
STARMDENRES: single
                                                                                          SOFTWARE: ASCII
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/747,863
                 COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: WINDOWS95
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
FEATURE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME/KEY: CDS
LOCATION: 11786..12532
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
LOCATION: 12394..13188
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME/KEY: CDS
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LOCATION: 12936..13484
OTHER INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FEATURE:
NAME/KEY: CDS
LOCATION: 7384..11772
OTHER INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NAME/KEY: CDS
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LOCATION: 13484..1
OTHER INFORMATION:
84111
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4 LeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15

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GENERAL INFORMATION:
APPLICANT: WILLIAM R. JACOBS AND GRAHAM F. HATFULL
TITLE OF INVENTION: D29 SHUTTLE PHASMIDS AND USES THEREOF
NUMBER OF SEQUENCES:
CORRESPONDENCE ADDRESS:
ADDRESSEE: AMSTER, ROTHSTEIN & EBENSTEIN
STREET: 90 PARK AVENUE
                                                                                                                                                                                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-614-770A-1
                                                                                                                                                                                                  12
Gaps: 0
Percent Identity: 66.667
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                                        Gaps: 0
Percent Identity: 46.667
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             COMPUTER READABLE FORM:
MEDIUM TYPE: 3.5 INCH 1.44 Mb STORAGE
MEDIUM TYPE: DISKETTE
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SOFTWARE: ASCII
CURRENT APPLICATION NOATA:
APPLICATION NUMBER: US/08/614,770A
FILING DATE: MARCH 7, 1996
ATOORNEY/AGENT INFORMATION:
NAME: ELIZABETH A. BOGOSIAN
REGISTRATION NUMBER: 39,911
REPERENCE/DEOKET NUMBER: 96700/402
TELEPHONE: (212) 697-5995
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPHONE: (212) 697-5995
TELEFAX: (212) 286-0854 or 286-0082
TELEX: TWX 710-581-4766
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                          seq_documentation_block:
; Sequence 1, Application US/08614770A
; Patent No. 5773267
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             alignment_block:
US-09-485-529-104 x US-08-614-770A-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGI.
MOLECULE TYPE:
DESCRIPTION: OLIGONUCLEOTIDE
                                                                                                 alignment_block:
US-09-485-529-104 x US-08-747-863-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ) ORGANISM: MYCOBACTERIOPHAGE;
INDIVIDUAL ISOLATE: D29
US-08-614-770a-1
                38.00
2.714
93.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      STATE: NEW YORK COUNTRY: U.S.A. ZIP: 10016
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NEW YORK
                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ANTI-SENSE: NO
ORIGINAL SOURCE
alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mohr, Christine
APPLICANT: Mondland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Resisting, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
                                                             seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-955
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Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPPERATING SYSTEM: PC-DOS/MS-DOS
SOFWWARE: Patentin Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REPERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPHONE: 919-541-8587
TELEFRAX: 919-541-8689
23802 CTCGCGCAGTTGGGCTACCGCGTAGAGGCTCTGAC 23837
                                                                                                                                                                                                                                                                                                                                                                                                                                        ADDRESSEE: No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
                                                                                                  eg_documentation_block:
Sequence 955, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_block:
US-09-485-529-104 x US-08-998-416-955
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   PRIOR APPLICATION DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    US-08-998-416-955
                                                                                                                                                                                                                                                                                                                                                                                                                                               STREET: 3054 Cornwallis Road
CTTY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           INFORMATION FOR SEQ ID NO: 955: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                             1152
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 640 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
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73.333
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CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PAG1590RP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FILING DATE: 24 CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Similarity:
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Quality:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ORGANISM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TELEFAX:
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APPLICANT: Pollinger, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mohr, Christine
APPLICANT: Mendland, Jurgen
APPLICANT: Kneedland, Jurgen
APPLICANT: Kneedland, Jurgen
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-1015
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER ENDABLE FORM:

MEDIUM TYPE: Floppy disk
COMPUTER: BIM PC compatible
COMPUTER: Floppy disk
COMPUTER: BIM PC compatible
COMPUTER: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSTRICATION: 435
PRIOR DATE: 24-DEC-1997
CLASSTRICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION:
TELECOMMUNICATION INFORMATION:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: No. 6239264artis Corporation
STREET: 3054 Cornwall1s Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  alignment_block:
US-09-485-529-104 x US-08-998-416-189/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Sequence 1015, Application US/08998416
Patent No. 6239264
GENERAL INFORMATION:
APPLICANT: Philippsen, Peter
APPLICANT: Polimann, Rainer
APPLICANT: Steiner, Sabine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         3.364
73.333
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY: linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_documentation_block:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                alignment_scores:
Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 27709
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ;
US-08-998-416-189
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                                                                                                                                                                                  APPLICANT: Philippsen, Peter
APPLICANT: Philippsen, Rainer
APPLICANT: Philippsen, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Mendland, Jurgen
APPLICANT: Mendland, Corinne
APPLICANT: Rechtle, Philipp
APPLICANT: AND USES THEREOF
CORRESPONDENCE ADDRESS: 1152
CORRESPONDENCE ADDRESS: 1152
ADDRESSEE: No. 6739264artis Corporation
STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STREET: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   to: 642
g_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-192
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       q_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-189
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPOTER: IEB PC compatible
COMPOTER: IEB PC compatible
COMPOTER: IEB PC compatible
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: DATA:
APPLICATION NUMBER: CH 0016/97
FILING DATE: 31-DEC-1996
ATTORNEY/AGENT INFORMATION:
NAME: MAL93 J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/COKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELECOMMUNICATION INFORMATION:
TELEFRANCE, 919-541-6869
INFORMATION FOR SEQ ID NO: 192:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 3 LeuteuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
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Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ignment_block:
S-09-485-529-104 x US-08-998-416-192/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     q_documentation_block:
Sequence 189, Application US/08998416
Patent No. 6239264
                                                                 q_documentation_block:
Sequence 192, Application US/08998416
Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic) ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     LENGTH: 642 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                3.364
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TOPOLOGY: linear
                                                                                                                                                                          GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Quality:
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ercent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY: U
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ignment_scores:
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NUMBER OF SEQUENCES: 1152
                                                                                                                                  COUNTRY: U
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                APPLICANT: Rebischung, Corinne
IITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
IITLE OF INVENTION: AND USES THEREOF
                                     APPLICANT: Rebisching, Corine
TITLE OF INVENTION: GENOMIC DNA SEQUENCES OF ASHBYA GOSSYPII
TITLE OF INVENTION: AND USES THEREOF
UNDRER OF SEQUENCES: 1152
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-386
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                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: Eloppy disk
COMPUTER: Eloppy disk
COMPUTER: TBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION NUMBER: CH 0016/97
FILING APPLICATION NUMBER: GT 0016/97
FILING DATE: 31-DEC-1996
ATTOMEX/AGERT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Percent Identity: 46.667
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             PF/5-30306/A/CGC1976
                                                                                                                                                       No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x US-08-998-416-1015/rev
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-:
TELECOMMUNICATION INFORMATION:
TELEPAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 1015:
SEQUENCE CHARACTERISTICS:
LENGTH: 718 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                       STREET: 3054 Cornwallis Road
CITY: Research Triangle Park
STATE: No. 6239264th Carolina
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Philippsen, Peter
Pohlmann, Rainer
Steiner, Sabine
Mohr, Christine
Wendland, Jurgen
Knechtle, Philipp
Wendland, Jurgen
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Ratio: 3.364
Percent Similarity: 73.333
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ORGANISM: PAG1622UP
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   linear
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: line
MOLECULE TYPE: D
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
Quality:
                                                                                                                                                                                                                                             USA
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APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
APPLICANT:
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to: 798
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-08-998-416-497
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         Align seg 1/1 to reverse of: US-08-998-416-386 from: 1
                                                                                                                                                                                                                                                             OUFTGATES PATENTIN Release #1.0, Version #1.30
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/998,416
FILING DATE: 24-DEC-1997
CLASSIFICATION: 435
PRIOR APPLICATION THORMATION:
APPLICATION NUMBER: 0006/97
FILING DATE: 31-DEC-1996
ATTONEY/AGENT INPORMATION:
NAME: Meigs, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
REFERENCE/DOCKET NUMBER: 38,241
RELEPRATION INFORMATION:
TELEFRANCE/DOCKET NUMBER: 39,241
RELEPRATION THORMATION:
TELEFRANCE/DOCKET NUMBER: 39,241
RELEPRATION OFFICE THORMATION:
TELEFRANCE/DOCKET NUMBER: 39,241
RELEPRATION OFFICE THORMATION:
TELEFRANCE/DOCKET NUMBER: 39,241
RELEPRATION OFFICE THORMATION:
TELEFRANCE/DOCKET NUMBER: 39,241
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Percent Identity: 46.667
ADDRESSEE: No. 6239264artis Corporation STREET: 3054 Cornwallis Road CITY: Research Triangle Park STATE: No. 6239264th Carolina COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             No. 6239264artis Corporation
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         APPLICANT: Philippsen, Peter
APPLICANT: Pohlmann, Rainer
APPLICANT: Steiner, Sabine
APPLICANT: Steiner, Sabine
APPLICANT: Wendland, Jurgen
APPLICANT: Knechtle, Philipp
APPLICANT: Rebischung, Corinne
TITLE OF INVENTION: GENOMIC DNA SEQUEN
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           alignment_block:
US-09-485-529-104 x US-08-998-416-386/rev
                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
; Sequence 497, Application US/08998416
; Patent No. 6239264
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CITY: Research Triangle Park
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        LENGTH: 798 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 INFORMATION FOR SEQ ID NO: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           NUMBER OF SEQUENCES: 1
CORRESPONDENCE ADDRESS:
ADDRESSEE: No. 62392
STREET: 3054 Cornwal
                                                                                                                                                                    COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 ; ORGANISM: PAG1292UP
US-08-998-416-386
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Percent Similarity:
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APPLICATION NUMBER: US 07/576,537
               19911217
                                                                                                                                                                                                                                                                                                                               TYPE: NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                                             linear
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                     STRANDEDNESS:
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                                                                                                                                                                                                                                                                                                                                                                                                                    US-07-809-457A-14
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Patent No. 5512466
GENERAL INFORMATION:
APPLICANT: Kishore, Ganesh M.
TITLE OF INVENTION: Control of Fruit Ripening and Senescence TITLE OF INVENTION: In Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-07-809-457A-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    362 CTGCTAAAACTACTCGGGTATCGAATCCGATTTGCTACTTTAGCC 406
                                                                                                                                                   CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
CLASSIFICATION:
APPLICATION NUMBER:
FILING APPLICATION
APPLICATION NUMBER:
FILING APPLICATION DATA:
APPLICATION NUMBER:
FILING DATE:
ATTORNEY/AGENT INFORMATION:
NAME: Me19s, J. Timothy
REGISTRATION NUMBER: 38,241
REFERENCE/DOCKET NUMBER: PF/5-30306/A/CGC1976
TELECOMMUNICATION INFORMATION:
TELEPRAN:
919-541-8689
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             3 LeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMetAla 17
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-998-416-497 from: 1 to: 832
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: PatentIn Release #1.0, Version #1.25 CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   APPLICATION NUMBER: US/07/809,457A
                                                                       COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-485-529-104 x US-08-998-416-497
No. 6239264th Carolina
:: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: 919-541-8689
INFORMATION FOR SEQ ID NO: 497:
SEQUENCE CHARACTERISTICS:
LENGTH: 832 base pairs
TYPE: nucleic acid
STRANDEDNESS: single
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
ORIGINAL SOURCE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            3.364
73.333
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MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        linear
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Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
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US-08-998-416-497
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TOPOLOGY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
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seq_documentation_block:
    Sequence 9, Application US/08476008
    Sequence 9, Application US/08476008
    Sequence No. 2627061
    Seberation: Application: Selfoling: Applicant: Kishore, Ganesh M.
    Applicant: Rishore, Ganesh M.
    Applicant: Stallings, William C.
    TITLE OF INVENTION: Glyphosate Tolerant
    TITLE OF INVENTION: Glyphosate Tolerant
    TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
    NUMBER OF SEQUENCES: 69
    CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  SSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
7: 700 Chesterfield Village Parkway
St. Louis
Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-476-008-9
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                              NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENGE/POCKET NUMBER: 38-21(10538)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-609
TELEPAX: (314)537-6047
INFORMATION.FOR SEQ ID NO: 14:
SEGUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
NAME: HOEFINE JF., Dennis R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x US-07-809-457A-14
                                                                                                                                                                                                                                                                                                                                                                                                        MOLECULE TYPE: DNA (genomic)
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3.083
85.714
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REFERENCE/DOCKET NUMBER: 38-21(10660)A
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Ratio:
Percent Similarity:
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Sequence 9, Application US/08306063
Sequence 9, Application US/08306063
Sequence 9, Application US/08306063
Setent No. 5633435
GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Rishore, Ganesh M.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: 61pphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               3: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 seg_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-306-063-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER: IBM PC Compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Align seg 1/1 to: US-08-476-008-9 from: 1 to: 1377
                                                                                                                  38-21(10660)A
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CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
            CLASSIFICATION: 435
ATTORNEY AGENT INFORMATION:
NAME: HOEINET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOOKET NUMBER: 38-21
TELECOMMUNICATION INFORMATION:
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 alignment_block:
US-09-485-529-104 x US-08-476-008-9
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                                                                                                                                                                                                                                                                                                                              ; TOPOLOGY: linear
; MOLECULE TYPE: DNA (genomic)
US-08-476-008-9
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FILING DATE: 31-AUG-1990
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Ratio: 3.083
Percent Similarity: 85.714
                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        COMPUTER READABLE FORM: MEDIUM TYPE: Floppy
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ADDRESSEE:
STREET: 70
                                                                                                                                                                                                                                                                                                                                                                                                                                                   alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COUNTRY:
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seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-553-943-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CURRENT APPLICATION DATA:

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/553,943

FILING DATE: 06-NOV-1995

CLASSIFICATION: 800

PRIOR APPLICATION NUMBER: US 07/809,457

FILING DATE: 17-DEC-1991

APPLICATION NUMBER: US 07/809,457

FILING DATE: 26-DEC-1990

ATTORNEY AGENT INFORMATION:

NAME: HOATHER JG. DENIER REFERENCE/DOCKET NUMBER: 30,914

REFERENCE/DOCKET NUMBER: 30,914

REFERENCE/DOCKET NUMBER: 30,914

REFERENCE/DOCKET NUMBER: 30,914

REFERENCE/DOCKET NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         1314 GATTTGATGGTCTTTGGAGCTAAGATCGAACTCTCCGAC 1355
                                                                                                                                                                                                                                                                                   Gaps: 14 Gaps: 0
                                                                                                                                                                                                                                                                                                                                                                                                                                                                        2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-306-063-9 from: 1 to: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           ADDRESSEE: Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
GITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            COMPUTER: IBM PC compatible OPERATING SYSTEM: PC-DOS/MS-DOS
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
TELEPHONE: (314)537-6047
TINFORMATION FOR SEQ ID NO: 9:
SEQUENCE CHARACTERISTICS:
LENGTH: 137 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
TYPE: TOPOLOGY: linear
US-08-306-063-9
                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x US-08-306-063-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEFAX: (314)537-6047 INFORMATION FOR SEQ ID NO:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: single
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US-08-833-485-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
APPLICANT: Kishore, Ganesh M.
APPLICANT: Padgette, Stephen R.
APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-833-485-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     COFTANTO STSTEM: PC-DOS/MS-DOS
COFTANTO STSTEM: PC-DOS/MS-DOS
CORRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/033,485
FILING DATE: U7-APR-1997
CLASSIFICATION: 435
PRIOR APPLICATION AAA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: A35
PRIOR APPLICATION: A35
PRIOR APPLICATION: A35
CLASSIFICATION: A35
PRIOR APPLICATION: A35
PRIOR APPLICATION NUMBER: US 07/576,537
PRIOR APPLICATION: A35
PRIOR APPLICATION: A35
PRIOR APPLICATION: A35
PRIOR APPLICATION NUMBER: US 07/576,537
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                1314 GATTIGATGGCTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 1355
                                                                                                                                                                                                             Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                            Align seg 1/1 to: US-08-553-943-14 from: 1 to: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                        2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY/AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
REPERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x US-08-553-943-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             seq_documentation_block:
; Sequence 9, Application US/08833485
; Patent No. 5804425
; MOLECULE TYPE: DNA (genomic)
US-08-553-943-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Floppy disk
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              CITY: St. Louis
STATE: Missouri
                                                                                                                                                     Quality:
Ratio:
Percent Similarity:
                                                                                                                         alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         COUNTRY:
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seq_documentation_block:
    Sequence 9, Application US/09137440
    Patent No. 6246876
    GENERAL INFORMATION:
    APPLICANT: Barry, Gerard F.
    APPLICANT: Rishore, Ganesh M.
    APPLICANT: Padgette, Stephen R.
    APPLICANT: Stallings, Willbarn C.
    TITLE OF INVENTION: Glyphosate Tolerant
    TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
    NUMBER OF SEQUENCES: 69
    CORRESPONDENCE ADDRESS:
    ADDRESSE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              E: Dennis R. Hoerner, Jr., Monsanto Co. BB4F 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-137-440-9
                                                                                                                                                                                                                                                                         Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
                                                                                                                                                                                                                                                2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                              Align seg 1/1 to: US-08-833-485-9 from: 1 to: 1377
                                                       Gaps:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              REFERENCE/DOCKET NUMBER: 38-21(15117)A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        FILING DATE:
CLASSIFICATION:
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/33,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION NUMBER: US 07/56,537
FILING DATE: 31-AUG-1990
FILING DATE: 31-AUG-1990
FILING DATE: 11-PRORMATION:
                                                                                                                          alignment_block:
US-09-485-529-104 x US-08-833-485-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              MOLECULE TYPE: DNA (genomic) US-09-137-440-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 9: SEQUENCE CHARACTERISTICS:
ENGTH: 1377 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       TELEPHONE: (314)737-6099
                                                    3.083
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                              37.00
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CITY: St. Louis
STATE: Missouri
COUNTRY: USA
ZIP: 63198
                                                                        Percent Similarity:
alignment_scores:
Quality:
                                                    Ratio:
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Fruit Ripening and Senescence
                                                                                                                    seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-09437-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-476-008-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1314 GATTTGATGGCTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 1355
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Align seg 1/1 to: PCT-US91-09437-14 from: 1 to: 1377
Align seg 1/1 to: PCT-US91-06148A-9 from: 1 to: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Length: 14
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/09437
FILING DATE: 19911217
                                        2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                                                                                                                                                                                                                700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      REFERENCE/DOCKET NUMBER: 38-21(10538)A TELECOMMUNICATION INFORMATION:
                                                                                                                                                                      Sequence 14, Application PC/TUS9109437
GENERAL INFORMATION:
APPLICANT: Klee, Harry J.
APPLICANT: Klshore, Ganesh M.
TITLE OF INVENTION: Control of Fruit
TITLE OF INVENTION: in Plants
NUMBER OF SEQUENCES: 17
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            FILING DATE: 19911217
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/632,440
FILING DATE: 26-DEC-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x PCT-US91-09437-14
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 14:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           GENERAL INFORMATION:
APPLICANT: Barry, Gerard F.
                                                                                                                                                                                                                                                                                                                                                 Monsanto Co.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      37.00
3.083
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                            ZIP: 63198
COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      NUCLEIC ACID
                                                                                                                                                                                                                                                                                                                                                              STREET: 700 Chesciff: St. Louis STATE: Missouri COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    linear
                                                                                                                                                              seq_documentation_block
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Quality:
Ratio:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE:
                                                                                                                                                                                                                                                                                                                                               ADDRESSEE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_scores:
                                                                                                                                                                                                                                                                                                                                         seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-06148A-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                            Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: PCT/US91/06148A
FILING DATE: 19910828
                                                                                                                                                                                                                         2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                                                                                               Align seg 1/1 to: US-09-137-440-9 from: 1 to: 1377
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: HOEFNET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10535)
TELECOMMUNICATION INFORMATION:
TELEFHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 9:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                FILING DATE: 19910828
CLASSIFICATION: 800
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US/07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        alignment_block:
US-09-485-529-104 x PCT-US91-06148A-9
                                                                                                                    alignment_block:
US-09-485-529-104 x US-09-137-440-9
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1377 base pairs
TYPE: NUCLEIC ACID
                                     37.00
3.083
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        37.00
3.083
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       COMPUTER READABLE FORM:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Percent Similarity:
                                                                         Percent Similarity:
                                          Quality:
Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    63198
                  alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   COUNTRY:
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APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                       ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-306-063-2
                                                                                                                                                                                                                                                                                                                                                                 SUCTIONE SISTEM: PC-LUDS/MS-DOS
SOCTIANES PATENTIN Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/476,008
FILING DATE: 07-JUN-1995
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
APPLICATION NUMBER: US 08/306,063
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
CLASSIFICATION: 435
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         PULGASIFICATION: 435
PULGATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: HOERNT INFORMATION:
REGISTRATION NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(10660)A
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       alignment_block:
US-09-485-529-104 x US-08-476-008-2
Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              LENGTH: 1982 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       CDS
62..1426
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                                                                                                                                                                                               CITY: St. Louis
STATE: Missouri
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                   USA
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US-08-476-008-2
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                                                                                                                                                                                                                                              COUNTRY:
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APPLICANT: Barry, Gerard F.

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APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-833-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           COMPUTER TOTALS

COMPUTER TEACHABLE FORM:

MEDIUM TYPE: Floppy disk

COMPUTER: IBM FOC. Compatible

OPERATING SYSTEM: PC-DOS/MS-DOS

SOFTWARE: Patentin Release #1.0, Version #1.25

CURRENT APPLICATION DATA:

APPLICATION NUMBER: US/08/306,063

FILING DATE: 13-SEP-1994

CLASSIFICATION: 435

PRIOR APPLICATION NUMBER: US 07/749,611

FILING DATE: 28-AUG-1991

CLASSIFICATION: 435

PRIOR APPLICATION DATA:

APPLICATION NUMBER: US 07/576,537

FILING DATE: 31-AUG-1990

CLASSIFICATION: WHERE: US 07/576,537

FILING DATE: 31-AUG-1990

CLASSIFICATION: A155

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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         seq_documentation_block:
    Sequence 2, Application US/08833485
    Setent No. 5804425
    GENERAL INFORMATION:
    APPLICANT: Barry, Gerard F.
    APPLICANT: Rishore, Ganesh M.
    APPLICANT: Padgette, Stephen R.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    alignment_block:
US-09-485-529-104 x US-08-306-063-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          ATTORNEY AGENT INFORMATION:
NAME: Hoerner Jr., Dennis R.
REGISTRATION NUMBER: 30,914
Kishore, Ganesh M.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TELEPHONE: (314)537-6099
TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            LENGTH: 1982 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      3.083
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                                                                                                                                                                                                                                                                                                                                                                                                          CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                Quality:
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, LOCATION:
US-08-306-063-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    COUNTRY:
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TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                        ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F STREET: 700 Chesterfield Village Parkway CITY: St. Louis STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-137-440-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               CURRENT APPLICATION DATA:
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/083,485
FILNG DATE: 07-APR 1997
CLASSIFICATION: 435
PRIOR APPLICATION ATA:
APPLICATION NUMBER: US/08/306,063
FILING DATE: 13-SEP-1994
CLASSIFICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION: 435
PRIOR APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
CLASSIFICATION: 435
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTONNEY/AGENT: NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
CLASSIFICATION: 435
ATTONNEY/AGENT: INFORMATION: DATA:
ANAME: LANGER OF THE PROPERTY O
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   Gaps: 0
Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    seq_documentation_block:
    Sequence 2, Application US/09137440
    Patent No. 6248876
    GENERAL INFORMATION:
    APPLICANT: Barry, Gerard F.
Stallings, William C.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_block:
US-09-485-529-104 x US-08-833-485-2
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       NAME: Hoerner Jr., Dennis R. REGISTRATION NUMBER: 30,914
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   REFERENCE/DOCKET NUMBER: 38
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)737-6099
TELEPAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 LENGTH: 1982 base pairs
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85.714
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STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                      ZIP: 63198
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy of
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     37.00
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                                                                                                                                                                                                                                                                                                                                                                                           USA
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US-08-833-485-2
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                                                                                                                                                                                                                                                                                                                                                                                      COUNTRY:
    APPLICANT:
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APPLICANT: Padgette, Stephen R.
APPLICANT: Stallings, William C.
TITLE OF INVENTION: Glyphosate Tolerant
TITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 69
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/PCTUS_COMB.seq:PCT-US91-06148A-2
                                                                                                                                         ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    Length: 14
Gaps: 0
Percent Identity: 50.000
                                                                                                                                                                                                                                                                                                                                                                          SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/137,440
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Align seg 1/1 to: US-09-137-440-2 from: 1 to: 1982
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REGISTRATION UNMBER: 30,914
REFERENCE/DOCKET NUMBER: 38-21(15117)A
TELECOMNUNICATION INFORMATION:
TELEPHORE: (314)737-6099
TELEFAX: (314)737-6047
INFORMATION FOR SEQ ID NO: 2:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 08/833,485
FILING DATE: 07-APR-1997
APPLICATION NUMBER: US 08/306,063
FILING DATE: 13-SEP-1994
PRIOR APPLICATION DATA:
APPLICATION NUMBER: US 07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION NUMBER: US 07/576,537
FILING DATE: 31-AUG-1990
ATTORNEY/AGENT INFORMATION:
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; Sequence 2, Application PC/TUS9106148A
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         alignment_block:
US-09-485-529-104 x US-09-137-440-2
                                                                                                                                                                                                                                                                               COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            APPLICANT: Barry, Gerard F.
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   SEQUENCE CHARACTERISTICS:
LENGTH: 1982 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                         OPERATING SYSTEM:
                                                                                                                                                                 STREET: 700 Chest
CITY: St. Louis
STATE: Missouri
COUNTRY: USA
                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              Quality:
Ratio:
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                                                                                                                                                                                                                                                            63198
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ; NAME/KEY:
; LOCATION:
US-09-137-440-2
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PAPELICANT: KUWABARA, YOKO
APPLICANT: HASHIGUCHI, Kenichi
APPLICANT: HASHIGUCHI, Kenichi
APPLICANT: HASHIGUCHI, Kenichi
APPLICANT: WARAMATSU, TSUYOSHI
APPLICANT: KURAHASHI, OSamu
APPLICANT: MORI, Yukiko
APPLICANT: ITO, Hisao
APPLICANT: ITO, Hisao
APPLICANT: ITO, Hisao
APPLICANT: BACTERIA AND METHOD FOR PRODUCING L-ARGININE
FILE REFERENCE: 0P945CIP
CURRENT APPLICATION NUMBER: US/09/629,616
CURRENT FILING DATE: 2000-07-31
NUMBER OF SEQ ID NOS: 7
SOSTWARE: PATENTIN VET: 2.0
    STREET: Steuart Street Tower, 20th Floor, One Market STREET: San Francisco
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-629-616-1
                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/08/106,761
FILING DATE: 19930813
CLASSIFICATION: 435
ATTORNEY/AGENT INFORMATION:
NAME: Weber, Kenneth A.
REFERENCE/DOCKET NUMBER: 2307E-445
TELECOMMUNICATION INFORMATION:
ADDRESSEE: TOWNSEND and TOWNSEND KHOURIE and CREW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Percent Identity: 61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       Align seg 1/1 to: US-08-106-761-1 from: 1 to: 2101
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   879 creecceaegcaegriaccegerccraecraregacare 917
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        4 LeuAlaAlaLeuGlyTyrLysValArgAlaSerAspMet 16
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_documentation_block:
   Sequence 1, Application US/09629616
   Patent No. 6255086
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x US-08-106-761-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             MOLECULE TYPE: DNA (genomic) HYPOTHETICAL: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  TELEPANE: (415) 543-9600
TELEFAX: (415) 543-5643
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 2101 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     ORGANISM: Homo sapiens
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       37.00
4.111
69.231
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      single
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                                                                                                               PRY: USA 94105
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Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       HYPOTHETICAL: NORIGINAL SOURCE:
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US-08-106-761-1
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      alignment_scores:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              FEATURE:
NAME/KEY:
                                                                                         STATE: C. COUNTRY:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         SOFTWARE:
SEQ ID NO 1
                APPLICANT: Padgette, Stephen R.

TITLE OF INVENTION: Glyphosate Tolerant
Glyphosate Tolerant
FITLE OF INVENTION: 5-Enolpyruvylshikimate-3-Phosphate Synthases
NUMBER OF SEQUENCES: 36
CORRESPONDENCE ADDRESS:
ADDRESSEE: Dennis R. Hoerner, Jr., Monsanto Co. BB4F
STREET: 700 Chesterfield Village Parkway
CITY: St. Louis
STATE: Missouri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           APPLICANT: HAMOCK, Bruce D.
APPLICANT: GRANT, David F.
APPLICANT: BEETHAM, Jeffrey K.
TITLE OF INVENTION: RECOMBINANT SOLUBLE EPOXIDE HYDROLASE NUMBER OF SEQUENCES: 14
CORRESPONDENCE ADDRESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-106-761-1
                                                                                                                                                                                                                                                                      COMPUTER FRADABLE FORM:
MEDIUM TYPE: Floppy disk
MEDIUM TYPE: Floppy disk
COMPUTER: EN PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PATENTIN DATA:
APPLICATION NUMBER: PCT/US91/06148A
FILING DATE: 19910828
CLASSIFICATION NUMBER: US/07/749,611
PRIOR APPLICATION NUMBER: US/07/749,611
FILING DATE: 28-AUG-1991
PRIOR APPLICATION NUMBER: US/07/749,611
FILING DATE: 31-AUG-1991
APPLICATION NUMBER: US/07/749,611
FILING DATE: 31-AUG-1990
ATTON NUMBER: US/07/576,537
FILING DATE: 31-AUG-1990
ATTONEX/AGENT INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        Align seg 1/1 to: PCT-US91-06148A-2 from: 1 to: 1982
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Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    NAME: HOEINET JT., Dennis R.
REGISTRATION NUMBER: 30,914
REPERENCE/DOCKET NUMBER: 38-21(10535)
TELECOMMUNICATION INFORMATION:
TELEPHONE: (314)537-6099
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                            alignment_block:
US-09-485-529-104 x PCT-US91-06148A-2
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; Sequence 1, Application US/08106761
; Patent No. 5445956
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           TELEFAX: (314)537-6047
INFORMATION FOR SEQ ID NO: 2:
SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               1982 base pairs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               37.00
3.083
85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                NUCLEIC ACID
EDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                62..1426
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APPLICANT: HAMMOCK
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Ratio:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           STRANDEDNESS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             Percent Similarity:
                                                                                                                                                                                                                                                       63198
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              alignment_scores:
APPLICANT:
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Patent No. 6204436
GENERAL INFORMATION:
APPLICANT:
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25 (EPO)
CURRENT APPLICATION DATA:
APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-5
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      Gaps: 0
Percent Identity: 50.000
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Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                              Align seg 1/1 to: US-09-629-616-1 from: 1 to: 4837
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|||||||:::::||||||||||::
4452 CTGGCGTCGATGGGCTACAAGATCCTCGCCACCGAA 4487
                    TYPE: DNA ORGANISM: Brevibacterium lactofermentum
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_documentation_block:
    Sequence 5, Application US/09182117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
; Sequence 1, Application US/09182117
; Patent No. 620436
; GENERAL INFORMATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     alignment_block:
US-09-485-529-104 x US-09-182-117-1
                                                                                                                                                                                                                                                                                                                                                                   US-09-485-529-104 x US-09-629-616-1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
LENGTH: 8012 base pairs
TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   3.083
                                                                                                        ; LOCATION: (283)..(1461)
; NAME/KEY: CDS
; LOCATION: (1470)..(4808)
US-09-629-616-1
                                                                                                                                                                                                                                                                                  Ratio:
Percent Similarity:
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                                                                                                                                                                                                                                                             Quality:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                 FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                HYPOTHETICAL:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      ; ANTI-SENSE:
US-09-182-117-1
                                                                                   NAME/KEY: CDS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                          alignment_scores:
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LENGTH: 4837
                                                                                                                                                                                                                                                                                                                                                 alignment_block:
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NUMBER OF SEQUENCES: 27
COMFUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: BM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
SOFTWARE: PatentIn Release #1.0, Version #1.25 (EPO)
APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SOFTWARE: Datentin Release #1.0, Version #1.25 (EPO) CURRENT APPLICATION DATA: APPLICATION NUMBER: US/09/182,117
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                              seq_name: /cgn2_6/ptodata/2/ina/6B_COMB.seq:US-09-182-117-4
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           2237 GATTTGATGGCTGGTCTTGGAGCTAAGATCGAACTCTCCGAC 2278
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Percent Identity: 50.000
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                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                    TITLE OF INVENTION: Transgenic Plant
NUMBER OF SEQUENCES: 27
COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC COMPATIBLE
OPERATING SYSTEM: PC-DOS/MS-DOS
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      seq_documentation_block:
; Sequence 4, Application US/09182117
; Patent No. 6204436
; GENERAL INFORMATION:
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US-09-485-529-104 x US-09-182-117-5
                                                                                                                                                                                                                                                                                                                                                                       TOPOLOGY: linear MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             TOPOLOGY: linear
MOLECULE TYPE: DNA (genomic)
                                                                                                                                                                                                                               CLASSIFICATION:
INFORMATION FOR SEQ ID NO: 5:
SEQUENCE CHARACTERISTICS:
LENGTH: 8418 base palrs
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                             INFORMATION FOR SEQ ID NO: 4: SEQUENCE CHARACTERISTICS:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           LENGTH: 8798 base pairs
                                                                                                                                                                                                                                                                                                                          TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                TYPE: nucleic acid
STRANDEDNESS: double
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                   FILING DATE:
CLASSIFICATION:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                           Quality:
Ratio:
Percent Similarity:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  ANTI-SENSE: NO
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                                                                                                                                                                                                              FILING DATE:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                        HYPOTHETICAL:
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alignment_scores:
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23905..24039, 24251..24418)
                                                                                                                                                                                                                                            seq_name: /cgn2_6/ptodata/2/ina/5A_COMB.seq:US-08-472-217-1
                                                                                                                                                                                                                                                                                                                                                                                                             APPLICANT: Jaakkola, Panu
APPLICANT: Jalkanen, Markku
APPLICANT: Lepp, Sirpa
APPLICANT: Mark ku
APPLICANT: Wark ku
APPLICANT: Vihinen, Tapani
APPLICANT: Wari, Anni
TITLE OF INVENTION: Syndecan Stimulation Of Cellular
TITLE OF INVENTION: Differentiation
CORRESPONDENCE: 4
CORRESPONDENCE ADDRESS:
                                                                                                                                                                            Percent Identity: 50.000
                                                                                                                                                        2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSerAsp 15
                                                                                                             to: 8798
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               PatentIn Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                         ADDRESSEE: Sterne, Kessler, Goldstein & Fox
STREET: 1100 New York Avenue, Suite 600
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      SUTREMENT PATCHIN RELEASE #1.0, Version CURRENT APPLICATION DATA:

APPLICATION NOWBER: US/08/472,217
FILING DATE: 07-JUN-1995
CLEASIFICATION 514
PRIOR APPLICATION DATA:
APPLICATION DATA:
APPLICATION DATA:
APPLICATION NUMBER: US 08/206,186
FILING DATE: 07-MAR-1994
PRIOR APPLICATION NUMBER: US 07/988,427
FILING DATE: 01-DEC-1992
ATTORNEY/AGENT INFORMATION:
NAME: Clinbala, Michale A.
REGISTRATION NUMBER: 33,851
REGISTRATION NUMBER: 33,851
TELECOMMUNICATION INFORMATION:
TELEPHONE: (202) 371-2600
INFORMATION FOR SEQ ID NO: 1:
SEQUENCE CHARACTERISTICS:
CHENCYL: SCATOU DASE PAIRS
CHENCYL: CASTOU DASE PAIRS
                                                                                                          Align seg 1/1 to: US-09-182-117-4 from: 1
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               COMPUTER: Floppy disk
COMPUTER: IBM PC compatible
OPERATING SYSTEM: PC-DOS/MS-DOS
SOGTWARE: Patentin Pal-
                                                                                                                                                                                                                                                                                                         Sequence 1, App\overline{1}1cation US/08472217 Patent No. 5726058
                                           alignment_block:
US-09-485-529-104 x US-09-182-117-4
                                                                                                                                                                                                                                                                                                                                                                           Alanen-Kurki, Leena
Auvinen, Petri
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MOLECULE TYPE: DNA (genomic)
HYPOTHETICAL: NO
ANTI-SENSE: NO
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                               TYPE: nucleic acid
STRANDEDNESS: hoth
Percent Similarity: 85.714
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                      COMPUTER READABLE FORM:
MEDIUM TYPE: Floppy
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                     STREET: 1100
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                20005
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APPLICANT:
APPLICANT:
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  CCATION:
COCATION:
US-08-472-217-1
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to: 26700
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    Sequence 5, Application US/08488199
    Patent No. 5851993
    Application:
    APPLICANT: Jalkanen, Markku
    ADPRESSEE: Jalkanen, Markanen
    ADPRESSEE: STERNE, KESSLER, GOLDSTEIN & FOX
    STREET: JALOO New YORK AVE., NW
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                  seq_name: /cgn2_6/ptodata/2/ina/5B_COMB.seq:US-08-488-199-5
                                                                                                                                                                                                                                                                                                Align seg 1/1 to reverse of: US-08-472-217-1 from: 1
                                                  Gaps: 0
Percent Identity: 61.538
                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                                       MEDIUM TYPE: Floppy disk
COMPUTER: IBM PC Compatible
OPERATURE: PSTSTEM: PC-DOS/MS-DOS
SOFTWARE: Patentin Release #1.0, Version #1.25
                                                                                                                                                                                                                                                                                                                                                                                                                                2 GluLeuLeuAlaAlaLeuGlyTyrLysValArgAlaSer 14
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CURRENT APPLICATION NUMBER: US/08/488,199
FILING DATE: 07-UNN-1995
CLASSIFICATION DATA:

APPLICATION NUMBER: US 08/258,862
FILING DATE: 13-UN-1994
ATTORNEY AFGENT INFORMATION:

NAME: Cimbala, Michele A.

REFERNCE/DOCKET NUMBER: 33,851
REFERNCE/DOCKET NUMBER: 1102.013000
TELEPHONE: 202-371-260

TELEPHONE: 202-371-260

TELEPHONE: 202-371-260

TELEPHONE: CONTROL ON SECULOR ON SECU
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US-09-485-529-104 x US-08-472-217-1/rev
37.00
3.700
76.923
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23905..24040
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24252..24418
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STRANDEDNESS: single
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STREET: 1100 ...
CITY: Washington
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Percent Similarity:
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COUNTRY: US
ZIP: 20005
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; LOCATION:
US-08-488-199-5
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alignment_scores:
Quality: 37.00 Length: 13
Ratio: 3.700 Gaps: 0
Percent Similarity: 76.923 Percent Identity: 61.538
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alignment\_block: US-09-485-529-104 x US-08-488-199-5/rev ..

Align seg 1/1 to reverse of: US-08-488-199-5 from: 1 to: 26700